

```
DR EMBL; AF364814; AAK83297.1; -.
DR EMBL; AF364815; AAK83298.1; -.
DR EMBL; AF364816; AAK83299.1; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS0017; DEATH DOMAIN; FALSE NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
KW Receptor; Developmental protein; Differentiation; Apoptosis;
KW Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 514
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER EDAR.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT DEATH.
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT M -> V (IN STRAIN HNI).
FT A -> P (IN STRAIN HNI).
FT S -> T (IN STRAIN HNI).
FT VARIANT 13 39
FT VARIANT 155 353
FT VARIANT 353 353
FT SEQUENCE 514 AA; 56066 MW; 82C7F0661EECFB48 CRC64;
SQ
Query Match 59.7%; Score 37; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQE 6
Db 51 CRPGQE 56

RESULT 12
YM80 YEAST
ID YM80 YEAST STANDARD; PRT; 515 AA.
AC Q03264;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 59.5 kDa protein in HDF1-MRPL33 intergenic region.
GN YMR285C OR YMR021.11C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Iye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XII."
RT Nature 387:90-93(1997).
RL Nature 387:90-93(1997).
CC -!- SIMILARITY: Belongs to the CCR4/nocturin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
```

```
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z49704; CAA89783.1; -.
DR PIR; S54592; S54592.
DR GenOnline; 142960; -.
DR SGD; S0004898; YMR285C.
DR GO; GO:0005622; C:intracellular; IDA.
DR GO; GO:0004521; F:endoribonuclease activity; IMP.
DR GO; GO:0006364; P:rRNA processing; IMP.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
KW Hypothetical protein.
SQ SEQUENCE 515 AA; 59539 MW; 89B30A7D24D6EBC8 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 515;
Best Local Similarity 47.1%; Pred. No. 28;
Matches 8; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 1 CR-----PGQELTKQG 11
Db 477 CRGFLRMPGNGENTKHG 493

RESULT 13
KCH8_MOUSE
ID KCH8_MOUSE STANDARD; PRT; 876 AA.
AC P59111;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 8 (Ether-a-go-go-
DE like potassium channel 3) (ELK3) (Fragment).
GN KCNH8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium
CC channel. Elicits a slowly activating, outward rectifying current
CC (By similarity). Channel properties may be modulated by cAMP and
CC subunit assembly (By similarity).
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or
CC heterotetrameric complex of pore-forming alpha subunits that can
CC associate with modulating beta subunits.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
```

```
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Bag)
CC subfamily.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; BC029690; AAH29690.1; -.
CC MGD; MGI:2445160; C130090D05Rik.
CC InterPro; IPR000595; CNMP_binding.
CC InterPro; IPR003967; Erg_Channel.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR005820; M+channel_nlg.
CC Pfam; PF00027; CNMP_binding; 1.
CC Pfam; PF00520; ion_trans; 1.
CC PRINTS; PR01470; ERGCHANNEL.
CC SMART; SM00100; CNMP; 1.
CC PROSITE; PS00888; CNMP_BINDING_1; FALSE_NEG.
CC PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.
CC PROSITE; PS50042; CNMP_BINDING_3; 1.
CC Transport; Ion transport; Ionic channel; Voltage-gated channel;
CC Potassium channel; Potassium; Potassium transport; Transmembrane;
CC Glycoprotein; Multigene family.
CC NON_TER 1 1
CC TRANSMEM <1 21 SEGMENT S1 (POTENTIAL).
CC TRANSMEM 30 50 SEGMENT S2 (POTENTIAL).
CC DOMAIN 51 72 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 73 93 SEGMENT S3 (POTENTIAL).
CC TRANSMEM 102 122 SEGMENT S4 (POTENTIAL).
CC DOMAIN 123 127 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 128 148 SEGMENT S5 (POTENTIAL).
CC DOMAIN 194 214 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
CC TRANSMEM 223 243 SEGMENT S6 (POTENTIAL).
CC DOMAIN 244 876 CYTOPLASMIC (POTENTIAL).
CC NP_BIND 325 442 CNMP.
CC DOMAIN 485 496 POLY-GLU.
CC CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 876 AA; 97486 MW; 83F60290F4C3FE0C CRC64;
CC -----
Query Match 59.7%; Score 37; DB 1; Length 876;
Best local Similarity 54.5%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC -----
QY 1 CRPQELTKQG 11
Db 346 CAPGEYLLRQG 356
CC -----
RESULT 14
Z445_MOUSE
ID Z445_MOUSE STANDARD; PRT; 986 AA.
AC Q8R2V3; Q8K216;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 445.
GN ZNF445.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
```

```
RA Zhou G., Wang J., Zhang Y.;
RT "Cloning of mouse zinc finger protein 445.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 345-986 FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: May be involved in transcriptional regulation.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -!- SIMILARITY: Contains 1 KRAB domain.
CC -!- SIMILARITY: Contains 1 SCAN box domain.
CC -!- SIMILARITY: Contains 12 C2H2-type zinc fingers.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AY341877; AAQ24161.1; -.
CC EMBL; BC027167; AAH27167.1; -.
CC EMBL; BC034572; AAH34572.1; ALT_INIT.
CC MGD; MGI:2143340; AW610627.
CC InterPro; IPR007087; Znf_C2H2.
CC Pfam; PF00096; zf-C2H2; 12.
CC SMART; SM00355; Znf_C2H2; 12.
CC PROSITE; PS50805; KRAB; 1.
CC PROSITE; PS50804; SCAN_BOX; 1.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
CC PROSITE; PS50157; ZINC_FINGER_C2H2_2; 12.
CC Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat.
FT DOMAIN 52 134 SCAN_BOX.
FT DOMAIN 219 289 KRAB.
FT ZN_FING 470 492 C2H2-TYPE 1.
FT ZN_FING 498 520 C2H2-TYPE 2.
FT ZN_FING 553 575 C2H2-TYPE 3.
FT ZN_FING 581 604 C2H2-TYPE 4.
FT ZN_FING 634 656 C2H2-TYPE 5.
FT ZN_FING 662 686 C2H2-TYPE 6.
FT ZN_FING 718 740 C2H2-TYPE 7.
FT ZN_FING 746 768 C2H2-TYPE 8.
FT ZN_FING 796 818 C2H2-TYPE 9.
FT ZN_FING 824 846 C2H2-TYPE 10.
FT ZN_FING 933 955 C2H2-TYPE 11.
FT ZN_FING 961 983 C2H2-TYPE 12.
FT CONFLICT 495 495 V -> L (IN REF. 2; AAH34572).
FT CONFLICT 709 709 R -> Q (IN REF. 2; AAH34572).
FT SEQUENCE 986 AA; 114774 MW; 26F5684634C32DFE CRC64;
SQ
```

Query Match 59.7%; Score 37; DB 1; Length 986;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQLTKQ 10
|||||:
Db 45 RPQQLFRQ 53

RESULT 15
Z445_HUMAN
ID Z445_HUMAN STANDARD; PRT; 1031 AA.
AC P59923;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 445.
GN ZNF445 OR ZNF168.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shan Y.X., Luo K.T., Guo Z.K., Tang W.W., Ye G.M., Yu L., Huang C.Q.;
RT "Cloning and characterization of a novel zinc finger protein."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in transcriptional regulation.
CC -!- SUBCELLULAR LOCATION: Nuclear (potential).
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
CC -!- SIMILARITY: Contains 1 KRAB domain.
CC -!- SIMILARITY: Contains 1 SCAN box domain.
CC -!- SIMILARITY: Contains 14 C2H2-type zinc fingers.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).

EMBL; AY262260; AAP36990.1; -;
DR EMBL; AY295873; AAP50258.1; -;
DR Genew; HGNC:21018; ZNF445.
DR PROSITE; PS50805; KRAB; 1.
DR PROSITE; PS50804; SCAN_BOX; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 14.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat.
FT DOMAIN 55 137 SCAN_BOX.
FT DOMAIN 234 304 KRAB.
FT ZN_FING 485 507 C2H2-TYPE 1.
FT ZN_FING 513 535 C2H2-TYPE 2.
FT ZN_FING 541 563 C2H2-TYPE 3.
FT ZN_FING 597 619 C2H2-TYPE 4.
FT ZN_FING 625 647 C2H2-TYPE 5.
FT ZN_FING 681 703 C2H2-TYPE 6.
FT ZN_FING 709 731 C2H2-TYPE 7.
FT ZN_FING 762 784 C2H2-TYPE 8.
FT ZN_FING 790 812 C2H2-TYPE 9.
FT ZN_FING 840 862 C2H2-TYPE 10.
FT ZN_FING 868 890 C2H2-TYPE 11.
FT ZN_FING 896 918 C2H2-TYPE 12.
FT ZN_FING 978 1000 C2H2-TYPE 13.
FT ZN_FING 1006 1028 C2H2-TYPE 14.
SQ SEQUENCE 1031 AA; 118962 MW; 39C2888028940063 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 1031;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQLTKQ 10
|||||:
Db 48 RPQQLFRQ 56

RESULT 16
KCH8_RAT
ID KCH8_RAT STANDARD; PRT; 1102 AA.
AC Q9QWS8; O88877;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 8 (Ether-a-go-go-like potassium channel 3) (ELK channel 3).
GN KCH8 OR ELK3 OR ELK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi W., Wang H.-S., Pan Z., Wymore R.S., Cohen I.S., McKinnon D.,
RA Dixon J.E.;
RT "Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in rat sympathetic ganglia."
RL J. Physiol. (Lond) 511:675-682(1998).
RN [2]
RP SEQUENCE OF 9-379 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=99043952; PubMed=9824707;
RA Engelard B., Neu A., Ludwig J., Roeper J., Pongs O.;
RT "Cloning and functional expression of rat ether-a-go-go-like K+ channel genes."
RL J. Physiol. (Lond) 513:647-654(1998).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=20183472; PubMed=10718922;
RA Wulfsen I., Hauber H.-P., Schiemann D., Bauer C.K., Schwarz J.R.;
RT "Expression of mRNA for voltage-dependent and inward-rectifying K channels in GH3/B6 cells and rat pituitary."
RL J. Neuroendocrinol. 12:263-272(2000).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=21319165; PubMed=11425889;
RA Saganich M.J., Machado E., Rudy B.;
RT "Differential expression of genes encoding subthreshold-operating voltage-gated K+ channels in brain."
RL J. Neurosci. 21:4609-4624(2001).
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits a slowly activating, outward rectifying current. Channel properties may be modulated by cAMP and subunit assembly. heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.
CC -!- SUBCELLULAR LOCATION: Detected in superior cervical, mesenteric and coeliac ganglia. Expressed in brain (piriform cortex, olfactory tubercle, cerebral cortex, hippocampus pyramidal cells and dentate gyrus and basal ganglia of caudate/putamen and accumbens nucleus). Expressed in pituitary.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF061957; AAC61520.1; -;
 DR EMBL; AJ007632; CAA07591.1; -;
 DR PIR; T17367; T17367.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR003967; Erg_Channel.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000700; PAS-assoc C.
 DR InterPro; IPR000014; PAS domain.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01470; ERGCHANNEL.
 DR SMART; SM00100; cNMP; 1.
 DR SMART; SM00086; PAC; 1.
 DR TIGRFAMS; TIGR00229; sensory box; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; FALSE NEG.
 DR PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.
 DR PROSITE; PS50042; CNMP_BINDING_3; 1.
 DR PROSITE; PS50113; PAC; 1.
 DR PROSITE; PS50112; PAS; FALSE NEG.
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 KW Glycoprotein; Multigene family.
 FT DOMAIN 1 225 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 226 246 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 256 276 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 277 298 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 299 319 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 328 348 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 349 353 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 354 374 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 420 440 SEGMENT H5 (POT-FORMING) (POTENTIAL).
 FT TRANSMEM 449 469 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 470 1102 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 18 90 PAS.
 FT DOMAIN 93 145 PAC.
 FT DOMAIN 711 722 POLY-GLU.
 FT NP BIND 551 668 CNMP.
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 71 71 F -> L (IN REF. 2).
 FT CONFLICT 187 187 K -> N (IN REF. 2).
 FT CONFLICT 296 296 I -> T (IN REF. 2).
 FT CONFLICT 370 370 M -> I (IN REF. 2).
 SQ SEQUENCE 1102 AA; 123230 MW; A135CC36E2E7F1A3 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 1102;
 Best Local Similarity 54.5%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 |||:|:|:
 Db 572 CAPGEYLLRQG 582

RESULT 17
 KCH8_HUMAN STANDARD; PRT; 1107 AA.
 ID KCH8_HUMAN
 AC Q96L42;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Potassium voltage-gated channel subfamily H member 8 (Ether-a-go-go-
 DE like potassium channel 3) (ELK channel 3) (ELK3) (ELK1) (hElk1).

GN KCNHB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21895915; PubMed=11897058;
 RA Baxter D.F., Kirk M., Garcia A.F., Raimondi A., Holmqvist M.H.,
 RA Flint K.K., Bojancic D., DiStefano P.S., Curtis R., Xie Y.;
 RT "A novel membrane potential-sensitive fluorescent dye improves
 RT cell-based assays for ion channels.";
 RL J. Biomol. Screen. 7:79-85 (2002).
 CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium
 CC channel. Elicits a slowly activating, outward rectifying current.
 CC Channel properties may be modulated by cAMP and subunit assembly.
 CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or
 CC heterotetrameric complex of pore-forming alpha subunits that can
 CC associate with modulating beta subunits.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -!- SIMILARITY: Belongs to the potassium channel family. H (Bag)
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AY053503; AAL15429.1; -;
 DR Genew; HGNC:18864; KCNHB.
 DR InterPro; IPR000595; cNMP_binding.
 DR InterPro; IPR003967; Erg_Channel.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000700; PAS-assoc C.
 DR InterPro; IPR000014; PAS domain.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01470; ERGCHANNEL.
 DR SMART; SM00100; cNMP; 1.
 DR SMART; SM00086; PAC; 1.
 DR TIGRFAMS; TIGR00229; sensory box; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; FALSE NEG.
 DR PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.
 DR PROSITE; PS50042; CNMP_BINDING_3; 1.
 DR PROSITE; PS50113; PAC; 1.
 DR PROSITE; PS50112; PAS; FALSE NEG.
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 KW Glycoprotein; Multigene family.
 FT DOMAIN 1 225 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 226 246 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 256 276 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 277 298 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 299 319 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 328 348 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 349 357 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 358 378 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 420 440 SEGMENT H5 (POT-FORMING) (POTENTIAL).
 FT TRANSMEM 449 469 SEGMENT S6 (POTENTIAL).

FT DOMAIN 470 1107 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 18 90 PAS.
FT DOMAIN 93 145 PAC.
FT DOMAIN 951 1064 SER-RICH.
FT DOMAIN 711 723 POLY-GLU.
FT NP BIND 551 668 CNMP.
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1107 AA; 123832 MW; 4DC93EF85B674905 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 1107;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRPGQELTKQG 11
Db 572 CAPGEYLLRQG 582

RESULT 18

FN1_MOUSE STANDARD; PRT; 2871 AA.
ID Q61554; Q60826;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrillin 1 precursor.
GN FN1 OR FN1-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95130561; PubMed=7829516;
RA Yin W., Germiller J., Sanguinetti C., Smiley E., Pangilinan T.,
RA Pereira L., Ramirez F., Bonadio J.,
RT "Primary structure and developmental expression of Fbn-1, the mouse
fibrillin gene."
RL J. Biol. Chem. 270:1798-1806(1995).
RN [2]

SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Structural component of connective tissue microfibrils
CC that binds calcium. Fibrillin-1-containing microfibrils provide
CC long-term force bearing structural support.
CC -!- PTM: Forms intermolecular disulfide bonds either with other
CC fibrillin-1 molecules or with other components of the microfibrils
CC (By similarity).
CC -!- SIMILARITY: Contains 47 EGF-like domains.
CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L29454; AAA56840.1; --
CC EMBL; U22493; AAA64217.1; --
CC PIR; A55624; A55624.
CC HSSP; P35555; LAPJ.
CC MGD; MGI:95489; Fbn1.
CC InterPro; IPR000152; Asx hydroxyl_s.
CC InterPro; IPR001881; EGF-Ca.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR002212; Fibril-assoc.
CC Pfam; PF00008; EGF; 45.
CC Pfam; PF00683; TB; 9.

DR SMART; SM00179; EGF CA; 42.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS00026; EGF_3; 45.
DR PROSITE; PS01187; EGF_CA; 43.
KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
Repeat; Signal; Multigene family.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 2871 FIBRILLIN 1.
FT DOMAIN 81 112 EGF-LIKE 1.
FT DOMAIN 115 146 EGF-LIKE 2.
FT DOMAIN 147 178 EGF-LIKE 3.
FT DOMAIN 246 287 EGF-LIKE 4.
FT DOMAIN 288 329 EGF-LIKE 5.
FT DOMAIN 330 401 TGFBP 1.
FT DOMAIN 402 446 PRO-RICH.
FT DOMAIN 449 489 EGF-LIKE 6.
FT DOMAIN 490 529 EGF-LIKE 7.
FT DOMAIN 530 571 EGF-LIKE 8.
FT DOMAIN 572 612 EGF-LIKE 9.
FT DOMAIN 613 653 EGF-LIKE 10.
FT DOMAIN 656 721 TGFBP 2.
FT DOMAIN 723 764 EGF-LIKE 11.
FT DOMAIN 765 806 EGF-LIKE 12.
FT DOMAIN 807 846 EGF-LIKE 13.
FT DOMAIN 910 951 EGF-LIKE 14.
FT DOMAIN 952 1018 TGFBP 3.
FT DOMAIN 1028 1069 EGF-LIKE 15.
FT DOMAIN 1070 1112 EGF-LIKE 16.
FT DOMAIN 1113 1154 EGF-LIKE 17.
FT DOMAIN 1155 1196 EGF-LIKE 18.
FT DOMAIN 1197 1237 EGF-LIKE 19.
FT DOMAIN 1238 1279 EGF-LIKE 20.
FT DOMAIN 1280 1321 EGF-LIKE 21.
FT DOMAIN 1322 1362 EGF-LIKE 22.
FT DOMAIN 1363 1403 EGF-LIKE 23.
FT DOMAIN 1404 1445 EGF-LIKE 24.
FT DOMAIN 1446 1486 EGF-LIKE 25.
FT DOMAIN 1487 1527 EGF-LIKE 26.
FT DOMAIN 1528 1599 TGFBP 4.
FT DOMAIN 1606 1647 EGF-LIKE 27.
FT DOMAIN 1648 1688 EGF-LIKE 28.
FT DOMAIN 1689 1758 TGFBP 5.
FT DOMAIN 1766 1807 EGF-LIKE 29.
FT DOMAIN 1808 1848 EGF-LIKE 30.
FT DOMAIN 1849 1890 EGF-LIKE 31.
FT DOMAIN 1891 1929 EGF-LIKE 32.
FT DOMAIN 1930 1972 EGF-LIKE 33.
FT DOMAIN 1973 2012 EGF-LIKE 34.
FT DOMAIN 2013 2054 EGF-LIKE 35.
FT DOMAIN 2055 2121 TGFBP 6.
FT DOMAIN 2127 2165 EGF-LIKE 36.
FT DOMAIN 2166 2205 EGF-LIKE 37.
FT DOMAIN 2206 2246 EGF-LIKE 38.
FT DOMAIN 2247 2290 EGF-LIKE 39.
FT DOMAIN 2291 2332 EGF-LIKE 40.
FT DOMAIN 2333 2400 TGFBP 7.
FT DOMAIN 2402 2443 EGF-LIKE 41.
FT DOMAIN 2444 2484 EGF-LIKE 42.
FT DOMAIN 2485 2523 EGF-LIKE 43.
FT DOMAIN 2524 2566 EGF-LIKE 44.
FT DOMAIN 2567 2606 EGF-LIKE 45.
FT DOMAIN 2607 2647 EGF-LIKE 46.
FT DOMAIN 2648 2687 EGF-LIKE 47.
FT DISULFID 85 94 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 102 111 BY SIMILARITY.
FT DISULFID 119 129 BY SIMILARITY.
FT DISULFID 123 134 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 150 160 BY SIMILARITY.
FT DISULFID 154 166 BY SIMILARITY.

FT	DISULFID	168	177	BY SIMILARITY.
FT	DISULFID	250	262	BY SIMILARITY.
FT	DISULFID	257	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	304	BY SIMILARITY.
FT	DISULFID	299	313	BY SIMILARITY.
FT	DISULFID	315	328	BY SIMILARITY.
FT	DISULFID	453	465	BY SIMILARITY.
FT	DISULFID	460	474	BY SIMILARITY.
FT	DISULFID	476	488	BY SIMILARITY.
FT	DISULFID	494	504	BY SIMILARITY.
FT	DISULFID	499	513	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	534	546	BY SIMILARITY.
FT	DISULFID	541	555	BY SIMILARITY.
FT	DISULFID	557	570	BY SIMILARITY.
FT	DISULFID	576	587	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
FT	DISULFID	598	611	BY SIMILARITY.
FT	DISULFID	617	628	BY SIMILARITY.
FT	DISULFID	623	637	BY SIMILARITY.
FT	DISULFID	639	652	BY SIMILARITY.
FT	DISULFID	727	739	BY SIMILARITY.
FT	DISULFID	734	748	BY SIMILARITY.
FT	DISULFID	750	763	BY SIMILARITY.
FT	DISULFID	769	781	BY SIMILARITY.
FT	DISULFID	776	790	BY SIMILARITY.
FT	DISULFID	792	805	BY SIMILARITY.
FT	DISULFID	811	821	BY SIMILARITY.
FT	DISULFID	816	830	BY SIMILARITY.
FT	DISULFID	832	845	BY SIMILARITY.
FT	DISULFID	914	926	BY SIMILARITY.
FT	DISULFID	921	935	BY SIMILARITY.
FT	DISULFID	937	950	BY SIMILARITY.
FT	DISULFID	1032	1044	BY SIMILARITY.
FT	DISULFID	1039	1053	BY SIMILARITY.
FT	DISULFID	1055	1068	BY SIMILARITY.
FT	DISULFID	1074	1086	BY SIMILARITY.
FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DISULFID	1097	1111	BY SIMILARITY.
FT	DISULFID	1117	1129	BY SIMILARITY.
FT	DISULFID	1124	1138	BY SIMILARITY.
FT	DISULFID	1140	1153	BY SIMILARITY.
FT	DISULFID	1159	1171	BY SIMILARITY.
FT	DISULFID	1166	1180	BY SIMILARITY.
FT	DISULFID	1182	1195	BY SIMILARITY.
FT	DISULFID	1201	1212	BY SIMILARITY.
FT	DISULFID	1208	1221	BY SIMILARITY.
FT	DISULFID	1223	1236	BY SIMILARITY.
FT	DISULFID	1242	1254	BY SIMILARITY.
FT	DISULFID	1249	1263	BY SIMILARITY.
FT	DISULFID	1265	1278	BY SIMILARITY.
FT	DISULFID	1284	1296	BY SIMILARITY.
FT	DISULFID	1291	1305	BY SIMILARITY.
FT	DISULFID	1307	1320	BY SIMILARITY.
FT	DISULFID	1326	1339	BY SIMILARITY.
FT	DISULFID	1333	1348	BY SIMILARITY.
FT	DISULFID	1350	1361	BY SIMILARITY.
FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DISULFID	1374	1389	BY SIMILARITY.
FT	DISULFID	1391	1402	BY SIMILARITY.
FT	DISULFID	1408	1420	BY SIMILARITY.
FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DISULFID	1431	1444	BY SIMILARITY.
FT	DISULFID	1450	1461	BY SIMILARITY.
FT	DISULFID	1456	1470	BY SIMILARITY.
FT	DISULFID	1472	1485	BY SIMILARITY.
FT	DISULFID	1491	1502	BY SIMILARITY.
FT	DISULFID	1497	1511	BY SIMILARITY.
FT	DISULFID	1513	1526	BY SIMILARITY.
FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	1617	1631	BY SIMILARITY.
FT	DISULFID	1633	1646	BY SIMILARITY.

Query Match

Best Local Similarity 59.7%; Score 37; DB 1; Length 2871;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy	1	CRPGQELTKQG 11
Db	1835	CKPGYRLTSTG 1845

RESULT 19

PEXC ARATH

ID PEXC ARATH STANDARD; PRT; 372 AA.

AC Q9M841;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Putative peroxisome assembly protein 12 (Peroxin-12).

GN AT3G04460 OR T27C4.11.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=21016720; PubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,

RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,

RA Delisny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA De Simone V., Choisme N., Artiguenave F., Robert C., Brothier P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,

RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bagues M., Terol J., Climent J.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,

RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,

RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,

RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,

RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis

thaliana.";

RL Nature 408:820-822(2000).

CC -!- FUNCTION: Required for protein import into peroxisomes (By

CC similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal

CC (Potential).

CC -!- SIMILARITY: Belongs to the peroxin 12 family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

```
DR EMBL; AC022287; AAF63777.1; -.
DR InterPro; IPR006845; Pex2_Pex12.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF04757; Pex2_Pex12; 1.
DR SMART; SM00184; RING; 1.
KW Hypothetical protein; Transmembrane; Peroxisome.
SQ SEQUENCE 372 AA; 41809 MW; 2ACAD19B27114A5 CRC64;

Query Match 58.9%; Score 36.5; DB 1; Length 372;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CR-PGQELTKQG 11
Db 234 CRATGQELTVQG 245

RESULT 20
RS4 ANASP
ID RS4 ANASP STANDARD; PRT; 202 AA.
AC Q8YTI0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S4.
GN RPSD OR RPS4 OR ALR2737.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the body of
CC the 30S subunit (By similarity).
CC -!- FUNCTION: With S5 and S12 plays an important role in translational
CC accuracy (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.
CC The interaction surface between S4 and S5 is involved in control
CC of translational fidelity (By similarity).
CC -!- SIMILARITY: Contains 1 S4 RNA-binding domain.
CC -!- SIMILARITY: Belongs to the S4P family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AP003590; BAB74436.1; -.
CC PIR; AB2148; AB2148.
CC HAMAP; MF_01306; -.
CC InterPro; IPR001912; Ribosomal_S4.
CC InterPro; IPR005709; Ribosomal_S4_b/o.
CC InterPro; IPR002942; S4.
CC Pfam; PF00163; Ribosomal_S4; 1.
CC Pfam; PF01479; S4; 1.
CC SMART; SM00363; S4; 1.
CC TIGRFAMs; TIGR01017; rpsD_bact; 1.
CC PROSITE; PS00632; RIBOSOMAL_S4; 1.
CC PROSITE; PS50889; S4; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
FT DOMAIN 90 152 S4 RNA-BINDING.

SQ SEQUENCE 202 AA; 23247 MW; E87CC650A4447229 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 202;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQEL 7
Db 131 CRPGEEI 137

RESULT 21
NCAP_VHSV0
ID NCAP_VHSV0 STANDARD; PRT; 404 AA.
AC P24378;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Viral hemorrhagic septicemia virus (strain 07-71) (VHSV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11288;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90362052; PubMed=2202782;
RA Bernard J., Lecocq-Xhonneux F., Rossius M., Thiry M.E.,
RA de Kinkelin P.;
RT "Cloning and sequencing the messenger RNA of the N gene of viral
haemorrhagic septicemia virus.";
RL J. Gen. Virol. 71:1669-1674(1990).
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: TO IHNV NUCLEOCAPSID PROTEIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D00687; BAA00591.1; -.
CC PIR; A36651; VHSVNS.
CC InterPro; IPR004902; Rhabdo_ncap_2.
CC Pfam; PF03216; Rhabdo_ncap_2; 1.
KW Nucleocapsid; Phosphorylation.
SQ SEQUENCE 404 AA; 44369 MW; 6C7200217ABA33A4 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 404;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPGQELTK 9
Db 184 RPGQKITK 191

RESULT 22
NCAP_VHSVM
ID NCAP_VHSVM STANDARD; PRT; 404 AA.
AC P27371;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Viral hemorrhagic septicemia virus (strain Makah) (VHSV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11289;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=92341050; PubMed=1634868;
RA Bernard J., Bremont M., Winton J.;
RT "Nucleocapsid gene sequence of a North American isolate of viral
RL haemorrhagic septicaemia virus, a fish rhabdovirus.";
RL J. Gen. Virol. 73:1011-1014(1992).
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: TO IHNV NUCLEOCAPSID PROTEIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X59241; CAA41930.1; -
DR PIR; JQ1531; JQ1531.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
KW Nucleocapsid; Phosphorylation.
SQ SEQUENCE 404 AA; 44066 MW; 54505A345B646DA1 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 404;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPOQELTK 9
Db 184 RPOQKITK 191

RESULT 23
EPB2_CHICK STANDARD; PRT; 1004 AA.
AC P28693;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor CEK5).
GN EPB2 OR CEK5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Embryo;
RX MEDLINE=92144672; PubMed=1664238;
RA Pasquale E.B.;
RT "Identification of chicken embryo kinase 5, a developmentally
RT regulated receptor-type tyrosine kinase of the Eph family.";
RL Cell Regul. 2:523-534(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Brain;
RX MEDLINE=93288394; PubMed=8510926;
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RL Oncogene 8:1807-1813(1993).
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN
CC IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; Synonyms=CEK5+;
CC IsoId=P28693-1; Sequence=Displayed;

Name=Short;
IsoId=P28693-2; Sequence=VSP_003018;
-!- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT
DEVELOPMENT AND SUSTAINED EXPRESSION IN ADULT BRAIN. THE LONGER
FORM (CEK5+) IS SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS
SYSTEM.
-!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
receptor subfamily.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; M62325; AAA48667.1; ALT_INIT.
PDB; 1SGG; 06-OCT-99.
InterPro; IPR006209; EGF like.
InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII subd.
InterPro; IPR008979; Gal_bind_like.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR001660; SAM.
InterPro; IPR001245; Tyr_kinase.
InterPro; IPR008266; Tyr_kinase_AS.
InterPro; IPR001426; YKase_receptorV.
Pfam; PF01404; EPH_lbd; 1.
Pfam; PF00041; fn3; 2.
Pfam; PF00059; pkinase; 1.
Pfam; PF00536; SAM; 1.
PRINTS; PR00014; FNTYPEIII.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS0105; SAM_DOMAIN; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
Repeat; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 1004
FT DOMAIN 20 544
FT TRANSMEM 545 565
FT DOMAIN 566 1004
FT DOMAIN 20 321
FT DOMAIN 326 419
FT DOMAIN 437 521
FT DOMAIN 639 902
FT DOMAIN 931 995
FT SITE 1002 1004
FT NP_BIND 645 653
FT BINDING 671 671
FT ACT_SITE 764 764
FT MOD_RES 614 614
FT MOD_RES 620 620
FT MOD_RES 798 798
FT MOD_RES 948 948
FT CARBOHYD 266 266
FT POTENTIAL.
FT EPHRIN TYPE-B RECEPTOR 2.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT CYS-RICH.
FT FIBRONECTIN TYPE-III 1.
FT FIBRONECTIN TYPE-III 2.
FT PROTEIN KINASE.
FT SAM.
FT PDZ-BINDING MOTIF (POTENTIAL).
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
```


RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edlmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.,
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [4]
RP SEQUENCE OF 374-578 FROM N.A.
RX MEDLINE=98409499; PubMed=9736772;
RA Laporte J.-L.;
RA Mandel J.-L.;
RT "Characterization of the myotubularin dual specificity phosphatase
RT gene family from yeast to human.";
RL Hum. Mol. Genet. 7:1703-1712(1998).
RN [5]
RP SEQUENCE OF 381-463 FROM N.A.
RX MEDLINE=96225444; PubMed=8640223;
RA Laporte J., Hu L.J., Kretz C., Mandel J.-L., Kioschis P., Coy J.,
RA Klauk S.M., Poutska A., Dahl N.;
RT "A gene mutated in X-linked myotubular myopathy defines a new
RT putative tyrosine phosphatase family conserved in yeast.";
RL Nat. Genet. 13:175-182(1996).
CC -!- FUNCTION: Dephosphorylates proteins phosphorylated on Ser, Thr,
CC and Tyr residues and low molecular weight phosphatase substrate
CC para-nitrophenylphosphate.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=B; Synonyms=FIVE-DSPib;
CC IsoId=Q13615-1; Sequence=Displayed;
CC Name=A; Synonyms=FIVE-DSPia;
CC IsoId=Q13615-2; Sequence=VSP_007781, VSP_007782;
CC Name=C; Synonyms=FIVE-DSPic;
CC IsoId=Q13615-3; Sequence=VSP_007781;
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. MYOTUBULARIN SUBFAMILY.
CC -!- SIMILARITY: Contains 1 FIVE-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF233436; AAF40203.2; -;
CC EMBL; AF233437; AAF40204.1; -;
CC EMBL; AF233438; AAF40205.1; -;
CC EMBL; AB002369; BAA20826.1; -;
CC EMBL; AC003071; AAB83949.1; -;
CC EMBL; U58034; AAC79119.1; -;
CC Genew; HGNC:7451; MIM:603558; -;
CC MIM; 603558; -;
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0016020; C:membrane; TAS.

DR GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.
DR GO; GO:0008138; F:protein tyrosine/serine/threonine phosphatase. .; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_Phosphatase.
DR InterPro; IPR000306; Znf_FYVE.
DR Pfam; PF01363; FYVE; 1.
DR SMART; SM00064; FYVE; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; FALSE_NEG.
DR PROSITE; PS0178; ZF_FYVE; 1.
KW Hydrolase; Zinc-finger; Alternative splicing.
FT ZN_FING 1119 1179 FIVE-TYPE.
FT ACT_SITE 413 413 SIMILARITY).
FT VARSPLIC 1076 1112 Missing (in isoform A and isoform C).
FT VARSPLIC 1142 1142 /FTId=VSP_007781.
FT CONFLICT 560 578 R -> RDTDRVDQTW (in isoform A).
FT CONFLICT 560 578 /FTId=VSP_007782.
FT SEQUENCE 1198 AA; 133618 MW; FE6F4B165074D5F8 CRC64;
SQ
QY 1 CRPGQELTKQ 10
DB 151 CRPGEHVTSR 160

RESULT 26
ATPZ_VIBAL
ID ATPZ_VIBAL STANDARD; PRT; 129 AA.
AC P12983;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATP synthase protein I.
GN ATP1 OR UNCI.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=138-2;
RX MEDLINE=90016889; PubMed=2529481;
RA Krumholz L.R., Esser U., Simoni R.D.;
RT "Nucleotide sequence of the unc operon of Vibrio alginolyticus.";
RL Nucleic Acids Res. 17:7993-7994(1989).
CC -!- FUNCTION: A possible function for this protein is to guide the
CC assembly of the membrane sector of the ATPase enzyme complex.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X16050; CAA34174.1; -;
CC PIR; S06075; S06075.
CC InterPro; IPR005598; ATP_synth_I.
CC Pfam; PF03899; ATP_synth_I; 1.
KW Hydrogen ion transport; CF(0); Transmembrane; Inner membrane.
FT TRANSMEM 16 36 POTENTIAL.

Query Match 58.1%; Score 36; DB 1; Length 1198;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

FT TRANSMEM 44 64 POTENTIAL.
FT TRANSMEM 77 97 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
SQ SEQUENCE 129 AA; 13835 MW; E376666CC1BE6C10 CRC64;
Query Match 56.5%; Score 35; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPQQLTKQ 10
Db 7 RPGLRLARQ 15
RESULT 27
EHC MYCTU STANDARD; PRT; 285 AA.
AC O53163;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable enoyl-CoA hydratase echA12 (EC 4.2.1.17).
GN ECHA12 OR FADB2 OR RV1472 OR MT1518 OR MTV007.19.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulterson J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).
CC -!- FUNCTION: COULD POSSIBLY OXIDIZES FATTY ACIDS USING SPECIFIC
CC COMPONENTS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: (3S)-3-hydroxyacyl-CoA = trans-2(or 3)-enoyl-
CC CoA + H(2)O.
CC -!- SIMILARITY: Belongs to the enoyl-CoA hydratase/isomerase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL021184; CAA16000.1; -.
DR EMBL; AE007021; AAK45783.1; -.
DR PIR; C70873; C70873.
DR HSSP; P14604; 2DUB.
DR TIGR; MT1518; -.

DR Tuberculist; RV1472; -.
DR InterPro; IPR001753; EnCoA_hydrase.
DR Pfam; PF00378; ECH; 1.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
KW Fatty acid metabolism; Lyase; Complete proteome.
SQ SEQUENCE 285 AA; 30575 MW; 6542FC79E7164F1C CRC64;
Query Match 56.5%; Score 35; DB 1; Length 285;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPQQLTKQ 10
Db 226 RPGLTLTKR 234
RESULT 28
NU2M ONCMY STANDARD; PRT; 349 AA.
AC P48175;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
GN MTND2 OR ND2.
OS Oncochrychus mykiss (Rainbow trout) (Salmo gairdneri).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncochrychus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96139027; PubMed=8587139;
RA Zardoya R., Garrido-Perterra A., Bautista J.M.;
RT "The complete nucleotide sequence of the mitochondrial DNA genome of
RT the rainbow trout, Oncochrychus mykiss."
RL J. Mol. Evol. 41:942-951 (1995).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L29771; AAB03348.1; -.
DR PIR; T09858; T09858.
DR InterPro; IPR003917; NADH_oxred2.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
DR PRINTS; PR01436; NADHDHGNASE2.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 349 AA; 37797 MW; 877DC34A237DADDF CRC64;
Query Match 56.5%; Score 35; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QELTKQG 11
Db 268 QELTKQG 274
RESULT 29
NU2M SALSAL STANDARD; PRT; 349 AA.
ID NU2M_SALSAL

```
AC Q35924; Q9MPEG9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
GN MTND2 OR ND2 OR NADH2 OR NADH-2.
OS Salmo salar (Atlantic salmon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20018174; PubMed=10548724;
RA Hurst C.D., Bartlett S.E., Davidson W.S., Bruce I.J.;
RT "The complete mitochondrial DNA sequence of the Atlantic salmon, Salmo
RT salar."
RL Gene 239:237-242(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Arnason U., Jonsson E., Rasmussen A.S.;
RT "The complete mitochondrial genome sequence of a teleost, Salmo salar,
RT and comparisons with other salmoniformes."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; U12143; AAD04734.1; -.
EMBL; AF133701; AAF61379.1; -.
PIR; T09948; T09948.
DR InterPro; IPR003917; NADHub_oxred2.
DR InterPro; IPR001750; Oxidored q1.
PFam; PF00361; oxidored q1; 1.
PRINETS; PR01436; NADHDHGNASE2.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
FT CONFLICT 79 79 W -> R (IN REF. 2).
SQ SEQUENCE 349 AA; 37853 MW; 1690A416D81B5358 CRC64;

Query Match 56.5%; Score 35; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11
Db 268 QELTKQG 274

RESULT 30
ARGD THEME
ID ARGD THEME STANDARD; PRT; 385 AA.
AC Q9X2A5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Acetylornithine aminotransferase (EC 2.6.1.11) (ACOAT).
GN ARGD OR TM1785.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
```

```
AC Q35924; Q9MPEG9;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
CC -!- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + 2-oxoglutarate = N-
CC acetyl-L-glutamate 5-semialdehyde + L-glutamate.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Arginine biosynthesis; fourth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- MISCELLANEOUS: May also have succinyldiaminopimelate
CC aminotransferase activity, thus carrying out the fourth step in
CC lysine biosynthesis.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; AE001816; AAD36848.1; -.
PIR; D72211; D72211.
DR HSSP; P04181; ZOAT.
DR TIGR; TM1785; -.
DR HAMAP; MF_01107; -.
DR InterPro; IPR005814; Aminotrans_3.
DR InterPro; IPR004636; ArgD.
PFam; PF00202; aminotran_3; 1.
DR TIGRFAMs; TIGR00707; argD; 1.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
KW Arginine biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate; Complete proteome.
FT BINDING 240 240 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 385 AA; 42884 MW; 4018F87FCBEFF60 CRC64;

Query Match 56.5%; Score 35; DB 1; Length 385;
Best Local Similarity 53.3%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 CRPG---QELTKQG 11
Db 276 CRAGTVIKELTKEG 290

RESULT 31
CIR_HUMAN
ID CIR_HUMAN STANDARD; PRT; 705 AA.
AC P00736;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Complement C1r component precursor (EC 3.4.21.41).
GN CIR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026566; PubMed=3021205;
RA Leytus S.P., Kurachi K., Sakariassen K.S., Davie E.W.;
RT "Nucleotide sequence of the cDNA coding for human complement C1r."
RT Biochemistry 25:4855-4863(1986).
```

[2] SEQUENCE FROM N.A., AND VARIANT LEU-152.
RX MEDLINE=87156625; PubMed=3030286;
RA Journet A., Tosi M.;
RT Cloning and sequencing of full-length cDNA encoding the precursor of
RT human complement component C1r.;
RL Biochem. J. 240:783-787(1986).
[3]
RP SEQUENCE OF 18-463.
RX MEDLINE=87241248; PubMed=3036070;
RA Arlaud G.J., Willis A.C., Gagnon J.;
RT "Complete amino acid sequence of the A chain of human complement-
RT classical-pathway enzyme C1r.";
RL Biochem. J. 241:711-720(1987).
[4]
RP SEQUENCE OF 464-705.
RX MEDLINE=83204782; PubMed=6303394;
RA Arlaud G.J., Gagnon J.;
RT "Complete amino acid sequence of the catalytic chain of human
RT complement subcomponent C1-r.";
RL Biochemistry 22:1758-1764(1983).
[5]
RP SEQUENCE OF 152-186, AND HYDROXYLATION.
RX MEDLINE=88005128; PubMed=2820791;
RA Arlaud G.J., van Dorsselaer A., Bell A., Mancini M., Aude C.,
RA Gagnon J.;
RT "Identification of erythro-beta-hydroxyasparagine in the EGF-like
RT domain of human C1r.";
RL FEBS Lett. 222:129-134(1987).
[6]
RP SEQUENCE OF 133-137; 187-211 AND 609-613, AND PHOSPHORYLATION.
RX MEDLINE=96221263; PubMed=8635594;
RA Pelloux S., Thielens N.M., Hudry-Clergeon G., Petillot Y., Filhol O.,
RA Arlaud G.J.;
RT "Identification of a cryptic protein kinase CK2 phosphorylation site
RT in human complement protease C1r, and its use to probe intramolecular
RT interaction.";
RL FEBS Lett. 386:15-20(1996).
[7]
RP STRUCTURE BY NMR OF 140-192.
RX MEDLINE=98138432; PubMed=9477945;
RA Bersch B., Hernandez J.-F., Marion D., Arlaud G.J.;
RT "Solution structure of the epidermal growth factor (EGF)-like module
RT of human complement protease C1r, an atypical member of the EGF
RT family.";
RL Biochemistry 37:1204-1214(1998).
CC -!- FUNCTION: C1r B chain is a serine protease that combines with C1q
CC and C1s to form C1, the first component of the classical pathway
CC of the complement system.
CC -!- CATALYTIC ACTIVITY: Selective cleavage of Lys(or Arg)-|-Ile bond
CC in complement subcomponent C1s to form the active form of C1s
CC (EC 3.4.21.42).
CC -!- SUBUNIT: C1 is a calcium-dependent trimolecular complex of C1q,
CC C1r and C1s in the molar ratio of 1:2:2. C1r is a dimer of
CC identical chains, each of which is activated by cleavage into two
CC chains, A and B, connected by disulfide bonds.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 2 Sushi (SCR) domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X04701; CAA38407.1; -.
CC EMBL; M14058; AAAS1851.1; -.
CC PIR; A24170; C1HURB.
CC PDB; 1APQ; 17-SEP-97.

PDB; 1GEZ; 31-JUL-02.
DR MEROPS; S01.192; -.
DR Genew; HGNC:1246; C1r.
DR MIM; 216950; -.
DR GO; GO:0003815; F:complement component C1r activity; TAS.
DR GO; GO:008236; F:serine-type peptidase activity; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; sushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Complement pathway; Plasma; Glycoprotein; Serine protease; Hydrolase;
KW Hydroxylation; Phosphorylation; Sushi; Repeat; Signal;
KW EGF-like domain; 3D-structure; Polymorphism.
FT SIGNAL 1 17
FT CHAIN 18 463 COMPLEMENT C1R HEAVY CHAIN.
FT CHAIN 464 705 COMPLEMENT C1R LIGHT CHAIN.
FT DOMAIN 18 141 CUB 1.
FT DOMAIN 142 190 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 193 305 CUB 2.
FT DOMAIN 308 372 SUSHI 1.
FT DOMAIN 375 448 SUSHI 2.
FT DOMAIN 464 705 SERINE PROTEASE.
FT ACT_SITE 502 502 CHARGE RELAY SYSTEM.
FT ACT_SITE 557 557 CHARGE RELAY SYSTEM.
FT ACT_SITE 654 654 CHARGE RELAY SYSTEM.
FT MOD_RES 167 167 HYDROXYLATION.
FT MOD_RES 206 206 PHOSPHORYLATION (BY CK2).
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .).
FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .).
FT DISULFID 71 89 PROBABLE.
FT DISULFID 146 165
FT DISULFID 161 174
FT DISULFID 176 189
FT DISULFID 193 220 PROBABLE.
FT DISULFID 250 268 PROBABLE.
FT DISULFID 309 358 PROBABLE.
FT DISULFID 338 371 PROBABLE.
FT DISULFID 376 429 PROBABLE.
FT DISULFID 406 447 PROBABLE.
FT DISULFID 451 577 INTERCHAIN (PROBABLE).
FT DISULFID 620 639 POTENTIAL.
FT DISULFID 650 680 POTENTIAL.
FT VARIANT 152 152 S -> L (in dbSNP:1801046).
FT TURN 145 147 /FTid=VAR_016103.
FT TURN 150 152
FT TURN 160 161
FT STRAND 164 168
FT TURN 169 170
FT STRAND 171 175

FT TURN 178 179
 FT STRAND 181 182
 FT TURN 184 185
 FT STRAND 189 190
 SQ SEQUENCE 705 AA; 80173 MW; 5CBCCCC0201061463 CRC64;

Query Match 56.5%; Score 35; DB 1; Length 705;
 Best Local Similarity 85.7%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQEL 7
 |||||
 Db 176 CRPGYEL 182

RESULT 32

MCM2 DROME STANDARD; PRT; 887 AA.
 ID MCM2 DROME STANDARD; PRT; 887 AA.

AC P49735; Q9VHU2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE DNA replication licensing factor MCM2.
 GN MCM2 OR CG7538.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE-antennal disk;
 RX MEDLINE=95347580; PubMed=7622035;
 RA Treisman J.E., Follette P.J., O'Farrell P.H., Rubin G.M.;
 RT "Cell proliferation and DNA replication defects in a Drosophila MCM2
 mutant.";
 RL Genes Dev. 9:1709-1715(1995).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: Acts as a factor that allows the DNA to undergo a single
 CC round of replication per cell cycle. Required for DNA replication
 CC and cell proliferation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: Belongs to the MCM family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----

EMBL; L42762; AAB36617.1; -.
 DR EMBL; AE003678; AAF54207.1; -.

DR FlyBase; FBgn0014861; Mcm2.
 DR InterPro; IPR001208; MCM.

DR InterPro; IPR008045; MCM_2.
 DR Pfam; PF00493; MCM; 1.

DR PRINTS; PR01657; MCMFAMILY.
 DR PRINTS; PR01658; MCMPROTEIN2.

DR ProDom; PD001041; MCM; 1.
 DR SMART; SMO0350; MCM; 1.

DR PROSITE; PS00847; MCM_1; 1.
 DR PROSITE; PS0051; MCM_2; 1.

KW Transcription regulation; DNA-binding; Nuclear protein;
 KW DNA replication; Zinc-finger; ATP-binding; Cell cycle.

FT ZN_FING 314 340 C4-TYPE (POTENTIAL).
 FT DOMAIN 458 665 MCM.

FT NP_BIND 508 515 ATP (POTENTIAL).
 SQ SEQUENCE 887 AA; 100414 MW; 26A7092109F09CBE CRC64;

Query Match 56.5%; Score 35; DB 1; Length 887;
 Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
 :|||

Db 391 CKPGDELEVTG 401

RESULT 33

RPOB BUCAP

ID RPOB BUCAP STANDARD; PRT; 1342 AA.

AC P41184;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase

DE beta chain) (RNA polymerase beta subunit).

GN RPOB OR BUSG035.

OS Buchnera aphidicola (subsp. Schizaphis graminum).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Buchnera.

OX NCBI_TaxID=98794;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93160925; PubMed=1369199;

RA Clark M.A., Baumann L., Baumann P.;

RT "Sequence analysis of an aphid endosymbiont DNA fragment containing

RT rpoB (beta-subunit of RNA polymerase) and portions of rplL and rpoC.";

RL Curr. Microbiol. 25:283-290(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22084549; PubMed=12089438;

RA Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,

RA Werngreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million Years of Genomic Stasis in Endosymbiotic Bacteria";
 RL Science 296:2376-2379(2002).
 CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC -!- CATALYTIC ACTIVITY: Nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -!- SUBUNIT: The enzyme consists of the sigma chain and the core
 CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
 CC beta' chain.
 CC -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z11913; CAA77970.1; --
 DR EMBL; AE014079; AAM67606.1; --
 DR PIR; S32680; S32680.
 DR HSSP; Q9KWU7; 1HQM.
 DR InterPro; IPR007121; RNA_pol_B.
 DR InterPro; IPR007644; RNA_pol_Rpb2_1.
 DR InterPro; IPR007642; RNA_pol_Rpb2_2.
 DR InterPro; IPR007645; RNA_pol_Rpb2_3.
 DR InterPro; IPR007120; RNA_pol_Rpb2_6.
 DR InterPro; IPR007641; RNA_pol_Rpb2_7.
 DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.
 DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.
 DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
 DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.
 DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
 DR PROSITE; PS01166; RNA_POL_BETA; 1.
 KW Transferase; Transcription; DNA-directed RNA polymerase;
 KW Complete proteome.
 SQ SEQUENCE 1342 AA; 152060 MW; 7E30BC9E013D31ED CRC64;

Query Match 56.5%; Score 35; DB 1; Length 1342;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQELTKQ 10
 Db 371 RPGEPLTKE 379

RESULT 34
 TENS CHICK
 ID TENS CHICK STANDARD; PRT; 1744 AA.
 AC Q04205; Q91007; Q92011;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Tensin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=94350987; PubMed=8071358;
 RA Lo S.H., An Q., Bao S., Wong W.K., Liu Y., Janney P.A., Hartwig J.H.,
 RA Chen L.B.;
 RT "Molecular cloning of chick cardiac muscle tensin. Full-length cDNA
 RT sequence, expression, and characterization.";
 RL J. Biol. Chem. 269:22310-22319(1994).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95204530; PubMed=7896874;
 RA Chuang J.Z., Lin D.C., Lin S.;
 RT "Molecular cloning, expression, and mapping of the high affinity
 RT actin-capping domain of chicken cardiac tensin.";
 RL J. Cell Biol. 128:1095-1109(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Chen L.B.;
 RA Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1469-1744 FROM N.A.
 RC TISSUE=Embryonic chondrocytes, and Embryonic heart;
 RX MEDLINE=94039118; PubMed=8223621;
 RA van de Werken R., Gennari M., Tavella S., Bet P., Molina F.,
 RA Lin S., Cancedda R., Castagnola P.;
 RT "Modulation of tensin and vimentin expression in chick embryo
 RT developing cartilage and cultured differentiating chondrocytes.";
 RL Eur. J. Biochem. 217:781-790(1993).
 RN [5]
 RP SH2 DOMAIN.
 RX MEDLINE=91220073; PubMed=1708917;
 RA Davis S., Lu M.L., Lo S.H., Lin S., Butler J.A., Druker B.J.,
 RA Roberts T.M., An Q., Chen L.B.;
 RT "Presence of an SH2 domain in the actin-binding protein tensin.";
 RL Science 252:712-715(1991).
 CC -!- FUNCTION: MAY BE INVOLVED IN CELL MIGRATION, CARTILAGE DEVELOPMENT
 CC AND IN LINKING SIGNAL TRANSDUCTION PATHWAYS TO THE CYTOSKELETON.
 CC BINDS TO ACTINS AND PHOSPHORYLATED PROTEINS IN SRC-TRANSFORMED
 CC CELLS. MAY BIND ACTIN WITH CAPPING AND BUNDLING PROPERTIES.
 CC -!- SUBCELLULAR LOCATION: LOCALIZES TO ADHERENS JUNCTIONS.
 CC -!- TISSUE SPECIFICITY: Heart, gizzard, lung and skeletal muscle.
 CC -!- PTM: Tyrosine phosphorylated.
 CC -!- SIMILARITY: Contains 1 tensin domain.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M96625; AAA59053.1; --
 DR EMBL; L06662; AAA73949.1; ALT_INIT.
 DR EMBL; Z18529; CAA79215.1; ALT_INIT.
 DR EMBL; M74165; AAA49087.1; --
 DR EMBL; X66286; CAA46992.1; --
 DR PIR; A54970; A54970.
 DR PIR; S27939; S27939.
 DR HSSP; P16277; 1BLK.
 DR InterPro; IPR008973; C2 CalB.
 DR InterPro; IPR006020; PTB_PID.
 DR InterPro; IPR000980; SH2.
 DR Pfam; PF00017; SH2; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00462; PTB; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 KW Actin-binding; Cytoskeleton; SH2 domain; Phosphorylation.
 FT DOMAIN 66 342
 FT DOMAIN 1472 1581
 FT CONFLICT 49 49
 FT CONFLICT 61 61
 FT CONFLICT 88 88
 FT CONFLICT 404 404
 FT CONFLICT 452 452
 FT CONFLICT 508 509
 FT CONFLICT 522 522
 FT CONFLICT 664 664
 FT CONFLICT 666 666
 FT C -> R (IN REF. 2).
 FT M -> T (IN REF. 2).
 FT Q -> P (IN REF. 3).
 FT A -> T (IN REF. 2).
 FT T -> A (IN REF. 2).
 FT DV -> EL (IN REF. 2).
 FT A -> P (IN REF. 2).
 FT R -> A (IN REF. 2).
 FT A -> T (IN REF. 2).

FT CONFLICT 875 875 P -> A (IN REF. 2).
FT CONFLICT 909 909 P -> T (IN REF. 2).
FT CONFLICT 1102 1113 MISSING (IN REF. 3).
FT CONFLICT 1240 1240 G -> A (IN REF. 2).
FT CONFLICT 1480 1480 E -> D (IN REF. 2).
FT CONFLICT 1711 1711 D -> E (IN REF. 2).
SQ SEQUENCE 1744 AA; 187214 MW; 5C3C8B6211935524 CRC64;

Query Match 56.5%; Score 35; DB 1; Length 1744;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PGQELTKQ 10
Db 25 PGQSITKQ 32

RESULT 35
LEG4_CHICK STANDARD; PRT; 134 AA.
AC P07583;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-galactoside-binding lectin (14 kDa lectin) (C-14).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86130505; PubMed=3004444;
RA Ohyama Y., Hirabayashi J., Oda Y., Ohno S., Kawasaki H., Suzuki K.,
RA Kasai K.-I.;
RT "Nucleotide sequence of chick 14K beta-galactoside-binding lectin
mRNA."
RL Biochem. Biophys. Res. Commun. 134:51-56 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89033999; PubMed=3182759;
RA Ohyama Y., Kasai K.-I.;
RT "Isolation and characterization of the chick 14K beta-galactoside-
binding lectin gene."
RL J. Biochem. 104:173-177 (1988).
RN [3]

RP SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=87250364; PubMed=3597352;
RA Hirabayashi J., Kawasaki H., Suzuki K., Kasai K.-I.;
RT "Complete amino acid sequence of 14 kDa beta-galactoside-binding
lectin of chick embryo."
RL J. Biochem. 101:775-783 (1987).
CC -!- FUNCTION: This protein binds beta-galactoside. Its physiological
function is not yet known. It may be involved in the regulation of
differentiation.
CC -!- SUBUNIT: Monomer (usually).
CC -!- TISSUE SPECIFICITY: Mainly in the intestine (adult), mainly in
the skin (embryo).
CC -!- SIMILARITY: Belongs to the galectin (galactin/S-lectin) family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M11674; AAA48779.1; -.
CC EMBL; D00311; BAA00214.1; -.
CC EMBL; D00308; BAA00214.1; JOINED.
CC EMBL; D00309; BAA00214.1; JOINED.

DR EMBL; D00310; BAA00214.1; JOINED.
DR PIR; JX0042; LNCH14.
DR HSP; P11116; ISLT.
DR InterPro; IPR008985; ConA_like_lect_gl.
DR InterPro; IPR01079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 1.
DR SMART; SM00276; GLECT; 1.
DR PROSITE; PS00309; GALAPTIN; 1.
KW Galectin; Lectin; Acetylation; Multigene family.
FT INIT MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT BINDING 69 75 BETA-GALACTOSIDE (POTENTIAL).
SQ SEQUENCE 134 AA; 14932 MW; 0F60E30C9A26B053 CRC64;

Query Match 54.8%; Score 34; DB 1; Length 134;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPOELTKQG 11
Db 13 KPGQRLTVKG 22

RESULT 36
IM23_SCHJA STANDARD; PRT; 218 AA.
ID IM23_SCHJA
AC P27591;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 23 kDa integral membrane protein (SJ23).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92140457; PubMed=1779990;
RA Davern K.M., Wright M.D., Herrmann V.R., Mitchell G.F.;
RT "Further characterisation of the Schistosoma japonicum protein Sj23,
a target antigen of an immunodiagnostic monoclonal antibody."
RL Mol. Biochem. Parasitol. 48:67-76 (1991).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M63706; AAA29920.1; -.
DR PIR; A40181; A40181.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PRO0259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Antigen; Transmembrane.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 36 POTENTIAL.
FT DOMAIN 37 55 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 71 POTENTIAL.
FT DOMAIN 72 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 108 POTENTIAL.
FT DOMAIN 109 183 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 184 205 POTENTIAL.
FT DOMAIN 206 218 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 218 AA; 23728 MW; C2AE75DD5B60F23A CRC64;

Query Match 54.8%; Score 34; DB 1; Length 218;
Best Local Similarity 54.5%; Pred. No. 41;


```
RL J. Bacteriol. 174:7585-7594 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
CC AFSQ1/AFSQ2 INVOLVED IN SECONDARY METABOLISM.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Phosphorylated by afsQ2 (Potential).
CC -!- SIMILARITY: Contains 1 response regulatory domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D10654; BAA01502.1; -.
DR EMBL; AL939121; CAC33072.1; -.
DR PIR; A45270; A45270.
DR HSSP; P08402; 1B00.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50110; RESPONSE REGULATORY; 1.
DR Phosphorylation; Transcription regulation; DNA-binding;
KW Sensory transduction; Complete proteome.
FT DOMAIN 1 116 RESPONSE REGULATORY.
FT MOD_RES 52 52 PHOSPHORYLATION (BY SIMILARITY).
FT MUTAGEN 52 52 D->E: LOSS OF PROTEIN'S ABILITY TO
FT STIMULATE ANTIBIOTIC PRODUCTION AND
FT PIGMENTATION.
FT CONFLICT 11 11 D -> E (IN REF. 1).
SQ SEQUENCE 225 AA; 25106 MW; 2834669A9F3F1E3E CRC64;

Query Match 54.8%; Score 34; DB 1; Length 225;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQLTKQ 10
Db 164 RPQQLSRQ 172

RESULT 39
TR18_HUMAN
ID TR18_HUMAN STANDARD; PRT; 241 AA.
AC Q9Y5U5; Q95851; Q9NYJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor).
GN TNFRSF18 OR GITR OR AITR.
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2 AND
RP TRAF3.
RC TISSUE=Bone marrow;
RX MEDLINE=99175482; PubMed=10074428;
RA Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
RA Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 9:215-218 (1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=T-cell;
RX MEDLINE=99156876; PubMed=10037686;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA Liu D., Wang S.-X., Kwon B.S.;
RT "Identification of a novel activation-inducible protein of the tumor
RT necrosis factor receptor superfamily and its ligand.";
RL J. Biol. Chem. 274:6056-6061 (1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Miglioni G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410 (2000).
CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y5U5-1; Sequence=Displayed;
CC Name=2; Synonyms=GITR-D;
CC IsoId=Q9Y5U5-2; Sequence=VSP_006508;
CC -!- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC leukocytes and weakly in spleen.
CC -!- INDUCTION: Upregulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF125304; AAD22635.1; -.
DR EMBL; AF117297; AAD19694.1; -.
DR EMBL; AF241229; AAF63506.1; -.
DR Genew; HGNC:11914; TNFRSF18.
DR MIM; 603905; -.
DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR TNFRSF18 OR GITR OR AITR.
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:21 ; Search time 3.76712 Seconds
(without alignments)
921.313 Million cell updates/sec

Title: US-10-067-122B-2_COPY_105_115
Perfect score: 62
Sequence: 1 CRPQELTKQG 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	211	11 Q8R037	Q8r037 mus musculu
2	43	69.4	880	4 Q8NAU9	Q8nau9 homo sapien
3	43	69.4	993	4 Q8IX30	Q8ix30 homo sapien
4	41	66.1	147	4 Q8IYY5	Q8iyy5 homo sapien
5	40	64.5	185	11 Q8BJS6	Q8bjs6 mus musculu
6	40	64.5	297	11 Q8BX35	Q8bx35 mus musculu
7	40	64.5	297	11 Q8BM50	Q8bm50 mus musculu
8	40	64.5	318	4 Q8IZA6	Q8iza6 homo sapien
9	40	64.5	379	16 Q87QQ8	Q87qq8 vibrio para
10	40	64.5	443	10 Q944J9	Q944j9 arabidopsis
11	40	64.5	459	10 Q9SF11	Q9sf11 arabidopsis
12	40	64.5	706	11 Q8CFG9	Q8cfg9 mus musculu
13	40	64.5	707	11 Q99KI6	Q99ki6 mus musculu
14	40	64.5	707	11 Q9ET60	Q9et60 mus musculu
15	40	64.5	707	11 Q8CG16	Q8cg16 mus musculu
16	40	64.5	2809	4 Q96JJP8	Q96jpp8 homo sapien

ALIGNMENTS

RESULT 1
Q8R037
ID Q8R037 PRELIMINARY; PRT; 211 AA.
AC Q8R037;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 9.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028507; AAH28507.1; -.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 1.

DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

KW Receptor.

SQ SEQUENCE 211 AA; 22452 MW; 1EECA84EA32A8D50 CRC64;

Query Match 100.0%; Score 62; DB 11; Length 211;
Best local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11

Db 105 CRPQELTKQG 115

RESULT 2

Q8NAU9

ID Q8NAU9 PRELIMINARY; PRT; 880 AA.
AC Q8NAU9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ34743.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamiyama K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AK092062; BAC03798.1; -.
DR Genew; HGNC:13655; CEGF3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recep.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001491; Thrombomoduln.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PRO0907; THROMBOMODULN.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_Ca; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_Ca; 3.
KW Hypothetical protein.
SQ SEQUENCE 880 AA; 97239 MW; F0BDE6E85266FD60 CRC64;
Query Match 69.4%; Score 43; DB 4; Length 880;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
QY 1 CRPGQELTK 9
Db 55 CRPGFELTK 63
||| |||
RESULT 3
Q8IX30 PRELIMINARY; PRT; 993 AA.
ID Q8IX30;
AC Q8IX30;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CUB and EGF containing protein.
GN CEGF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Pfarr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R.,
RA Harkeln T., Winterpacht A.;
RT "Novel human gene family (CEGF) encoding mosaic proteins with EGF-
RT like, SFT2R and a CUB module: cloning and expression analysis."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452494; AAN76808.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recep.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 9.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 10.
DR SMART; SM00179; EGF_Ca; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_Ca; 6.
SQ SEQUENCE 993 AA; 109282 MW; 19BBE0E5627EEAF4 CRC64;
Query Match 69.4%; Score 43; DB 4; Length 993;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRPGQELTK 9
Db 184 CRPGFELTK 192
||| |||
RESULT 4
Q8IYY5 PRELIMINARY; PRT; 147 AA.
ID Q8IYY5;
AC Q8IYY5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033292; AAH33292.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR008957; FN_III-like.
KW Hypothetical protein.
SQ SEQUENCE 147 AA; 16945 MW; 71BAF49274618999 CRC64;
Query Match 66.1%; Score 41; DB 4; Length 147;
Best Local Similarity 70.0%; Pred. No. 7.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RPQGELTKQG 11
Db 93 RPQMEITKDG 102
||| |||
RESULT 5
Q8BJS6 PRELIMINARY; PRT; 185 AA.
ID Q8BJS6;
AC Q8BJS6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to X-linked ectodysplasin-A receptor.
GN XEDAR OR 9430060M22RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK080072; BAC37822.1; -.
DR MGD; MGI:2442860; Xedar.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 185 AA; 20832 MW; 7335CCAC83C829C4 CRC64;

Query Match 64.5%; Score 40; DB 11; Length 185;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
| | | | | | | |
Db 21 CGPGQELSK 29

RESULT 6
Q8BX35
ID Q8BX35 PRELIMINARY; PRT; 297 AA.
AC Q8BX35;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to X-linked ectodysplasin-A receptor.
GN XEDAR OR 9430060M22RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK049134; BAC33562.1; -.
DR MGD; MGI:2442860; Xedar.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 297 AA; 33066 MW; 46FEFDDC51D739BE CRC64;

Query Match 64.5%; Score 40; DB 11; Length 297;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
| | | | | | | |
Db 21 CGPGQELSK 29

Db 21 CGPGQELSK 29

RESULT 7
Q8BM50
ID Q8BM50 PRELIMINARY; PRT; 297 AA.
AC Q8BM50;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to X-linked ectodysplasin-A receptor.
GN XEDAR OR 9430060M22RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK034909; BAC28879.1; -.
DR MGD; MGI:2442860; Xedar.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 297 AA; 33038 MW; D5F2CD188765AD65 CRC64;

Query Match 64.5%; Score 40; DB 11; Length 297;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
| | | | | | | |
Db 21 CGPGQELSK 29

RESULT 8
Q8IZA6
ID Q8IZA6 PRELIMINARY; PRT; 318 AA.
AC Q8IZA6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE X-linked ectodermal dysplasia receptor long isoform.
GN XEDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22323314; PubMed=12270937;
RA Sinha S.K., Zachariah S., Quinones H.I., Shindo M., Chaudhary P.M.;
RT "Role of TRAF3 and -6 in the Activation of the NF-kappa B and JNK
RT Pathways by X-linked Ectodermal Dysplasia Receptor.";
RL J. Biol. Chem. 277:44953-44961 (2002).
DR EMBL; AY152724; AAN73210.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 318 AA; 34992 MW; A4C8AED32F346A3E CRC64;

Query Match 64.5%; Score 40; DB 4; Length 318;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
 |||||
 Db 21 CGPGQELSK 29

RESULT 9
 Q87QQ8 PRELIMINARY; PRT; 379 AA.

ID Q87QQ8
 AC Q87QQ8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative transmembrane protein affecting septum formation and cell
 DE membrane permeability.
 GN VP1091.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 RT distinct from that of V. cholerae."
 RL Lancet 361:743-749(2003).
 DR EMBL: AP005076; BAC59354.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008565; F:protein transporter activity; IEA.
 DR GO; GO:0009306; P:protein secretion; IEA.
 DR InterPro; IPR006143; HlyD.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR Pfam; PF00529; HlyD; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Transmembrane; Complete proteome.
 SQ SEQUENCE 379 AA; 40389 MW; 97938BB9E2268CDB CRC64;

Query Match 64.5%; Score 40; DB 16; Length 379;
 Best Local Similarity 63.6%; Pred. No. 32;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11
 |||||
 Db 20 CQPSQEGTEQ 30

RESULT 10
 Q944J9 PRELIMINARY; PRT; 443 AA.

ID Q944J9
 AC Q944J9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE AT3G1180/F26K24.17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; Tissue=Accessory reproductive organs;
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF428353; AAL16283.1; -
 SQ SEQUENCE 443 AA; 49596 MW; 6FFB2BB1673607C1 CRC64;

Query Match 64.5%; Score 40; DB 10; Length 443;
 Best Local Similarity 70.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 10
 |||||
 Db 286 CEPGSELMKQ 295

RESULT 11
 Q9SF11 PRELIMINARY; PRT; 459 AA.

ID Q9SF11
 AC Q9SF11;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE F26K24.17 protein.
 GN F26K24.17;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC F26K24 genomic sequence."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC016795; AAF23204.1; -
 SQ SEQUENCE 459 AA; 51414 MW; CE994D766025B8F9 CRC64;

Query Match 64.5%; Score 40; DB 10; Length 459;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 10
 |||||
 Db 302 CEPGSELMKQ 311

RESULT 12
 Q8CFG9 PRELIMINARY; PRT; 706 AA.

ID Q8CFG9
 AC Q8CFG9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Complement component C1RB.
 GN C1R OR C1RB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; Tissue=Accessory reproductive organs;
 RA Garnier G., Circolo A., Xu Y., Volanakis J.E.;
 RT "The murine C1r/C1s gene cluster."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF459018; AAC15557.1; -
 DR MGD; MGI:1355313; C1r.

DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 707 AA; 80142 MW; CC90F1163A52D824 CRC64;

Query Match 64.5%; Score 40; DB 11; Length 707;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
| | | | |
Db 175 CHPGYELQKDG 185

RESULT 15
Q8CG16 PRELIMINARY; PRT; 707 AA.
AC Q8CG16;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Complement component C1ra.
GN C1RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Garnier G., Circolo A., Xu Y., Volanakis J.E.;
RT "The murine C1r/C1s gene cluster";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF459011; AA015553.1; -
DR EMBL; AF459008; AA015553.1; JOINED.
DR EMBL; AF459009; AA015553.1; JOINED.
DR EMBL; AF459010; AA015553.1; JOINED.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; sushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 707 AA; 80073 MW; 29DAAEB3C047D8E8 CRC64;

Query Match 64.5%; Score 40; DB 11; Length 707;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
| | | | |
Db 175 CHPGYELQKDG 185

RESULT 16
Q96JPS PRELIMINARY; PRT; 2809 AA.
AC Q96JPS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibrillin3.
GN KIAA1776.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro";
RL DNA Res. 8:85-95(2001).
DR EMBL; AB053450; BAB47408.1; -
DR Genbank; HGNC:18794; FBN3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 42.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00179; EGF_CA; 41.
DR PROSITE; PS00010; ASX_HYDROXYL; 41.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 36.
DR PROSITE; PS01187; EGF_CA; 40.
KW EGF-like domain.
SQ SEQUENCE 2809 AA; 300323 MW; 20C04CC006C0161F CRC64;

Query Match 64.5%; Score 40; DB 4; Length 2809;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
| | | | |
Db 1098 CPPGHETAKG 1108

RESULT 17
Q86SJS PRELIMINARY; PRT; 2809 AA.
AC Q86SJS;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibrillin-3 short form precursor transcript variant 1 (Fibrillin-3
DE short form precursor transcript variant 2) (Fibrillin-3 short form
DE precursor transcript variant 3).
GN FBN3.

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Corson G.M., Charbonneau N.L., Keene D.R., Sakai L.Y.;
RT "A Third Fibrillin Adds Diversity to Extracellular Microfibrils.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY165863; AAO18145.1; -.
DR EMBL; AY165864; AAO18146.1; -.
DR EMBL; AY165865; AAO18147.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; Asx hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 45.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00181; EGF; 46.
DR SMART; SM00179; EGF_CA; 43.
DR PROSITE; PS00010; ASX_HYDROXYL; 41.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 36.
DR PROSITE; PS01187; EGF_CA; 40.
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 48 2689 FIBRILLIN-3 SHORT FORM.
FT SEQUENCE 2809 AA; 300367 MW; 064F6FFB8B239473 CRC64;
SQ
Query Match 64.5%; Score 40; DB 4; Length 2809;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
|:|:|:|:|
Db 1098 CPGGHETAKG 1108

RESULT 18
Q8C4K3 PRELIMINARY; PRT; 250 AA.
AC Q8C4K3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor superfamily.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK081878; BAC38357.1; -.
DR MGD; MGI:894675; Tnfrsf18.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00208; TNFR; 2.
SQ SEQUENCE 250 AA; 27814 MW; 6963E94F414C16B4 CRC64;

Query Match 62.9%; Score 39; DB 11; Length 250;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CRPGQELTKQG 11
|:|:|:|:|
Db 82 CQPGQRVESQG 92

RESULT 19
Q88JD7 PRELIMINARY; PRT; 213 AA.
AC Q88JD7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved domain protein.
GN PP2712.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016784; AAN68320.1; -.
DR TIGR; PP2712; -.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
KW Complete proteome.
SQ SEQUENCE 213 AA; 23480 MW; 6E89CB3C04EBC420 CRC64;
```

```
Query Match 61.3%; Score 38; DB 16; Length 213;
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 RFGQELTKQG 11
|:|:|:|:|
Db 187 RFGRELADQG 196

RESULT 20
Q82036 PRELIMINARY; PRT; 249 AA.
AC Q82036;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8401-H;
RA Nishizawa T.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D45422; BAA08261.1; -.
DR GO; GO:0019013; C:viral nucleocapsid; IEA.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 249 AA; 26936 MW; 52FF2BFA5D47DB89 CRC64;
```

```

Query Match          61.3%; Score 38; DB 12; Length 249;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPOQELTK 9
Db 39 RPOQKLTk 46

RESULT 21
Q9H9A3
ID Q9H9A3 PRELIMINARY; PRT; 307 AA.
AC Q9H9A3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ12892.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022954; BAB14329.1; -.
KW Hypothetical protein.
SQ SEQUENCE 307 AA; 33374 MW; 6833080C0808B9833 CRC64;

Query Match          61.3%; Score 38; DB 4; Length 307;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
Db 15 CKPGNLTk 23

RESULT 22
Q08449
ID Q08449 PRELIMINARY; PRT; 391 AA.
AC Q08449;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Infectious hematopoietic necrosis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11290;
RN [1]
RP SEQUENCE FROM N.A.
RA Schuetze H., Enzmann P.J., Kuchling R., Mundt E., Niemann H.,
RA Mettenleiter T.C.;
RL J. Gen. Virol. 14:2519-2527(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=X;
RA Schuetze H.;
RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=X;
RX MEDLINE=89073771; PubMed=3201758;
RA Gilmore R.D., Leong J.C.;
RT "The nucleocapsid gene of infectious hematopoietic necrosis virus, a
fish rhabdovirus.";
```

```

Virology 167:644-648(1988).
-!- PTM: PHOSPHORYLATED (BY SIMILARITY).
-!- SIMILARITY: TO VHSV NUCLEOCAPSID PROTEIN.
DR EMBL; X73872; CAA52071.1; -.
DR EMBL; X89213; CAA61495.1; -.
DR GO; GO:0019013; C: viral nucleocapsid; IEA.
DR GO; GO:0006457; P: protein folding; IEA.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
KW Nucleocapsid; Phosphorylation.
SQ SEQUENCE 391 AA; 42309 MW; 88FF0C5E2E03D32B CRC64;

Query Match          61.3%; Score 38; DB 12; Length 391;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPOQELTK 9
Db 183 RPOQKLTk 190

RESULT 23
Q82680
ID Q82680 PRELIMINARY; PRT; 391 AA.
AC Q82680;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleocapsid protein.
GN N GENE.
OS Infectious hematopoietic necrosis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11290;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WRAC;
RX MEDLINE=96118173; PubMed=8578857;
RA Morzunov S.P., Winton J.R., Nichol S.T.;
RT "The complete genome structure and phylogenetic relationship of
infectious hematopoietic necrosis virus.";
RL Virus Res. 38:175-192(1995).
DR EMBL; L40883; AAC42150.1; -.
DR GO; GO:0019013; C: viral nucleocapsid; IEA.
DR GO; GO:0006457; P: protein folding; IEA.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
SQ SEQUENCE 391 AA; 42208 MW; 959C930C0C080E55D8 CRC64;

Query Match          61.3%; Score 38; DB 12; Length 391;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPOQELTK 9
Db 183 RPOQKLTk 190

RESULT 24
Q82679
ID Q82679 PRELIMINARY; PRT; 391 AA.
AC Q82679;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleoprotein.
GN N.
OS Infectious hematopoietic necrosis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
```

```
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11290;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Round Butte 1;
RA Emmenegger E.J., Kurath G.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50402; AAA97895.1; -.
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 391 AA; 42073 MW; 7F9F11640AA7AA6D CRC64;

Query Match 61.3%; Score 38; DB 12; Length 391;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQQLTK 9
Db 183 RPQQLTK 190

RESULT 25
Q9QL89 PRELIMINARY; PRT; 392 AA.
AC Q9QL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA 9703;
RA Oh H.K., Choi T.J.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104985; AAF14116.1; -.
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;

Query Match 61.3%; Score 38; DB 12; Length 392;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQQLTK 9
Db 182 RPQQLTK 189

RESULT 26
Q9UFH0 PRELIMINARY; PRT; 417 AA.
AC Q9UFH0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFP2P434L1050.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
```

```
DR EMBL; AL122079; CAB59254.1; -.
DR PIR; T34561; T34561.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 417 AA; 46334 MW; 1369AA2D69578BA6 CRC64;

Query Match 61.3%; Score 38; DB 4; Length 417;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
Db 125 CKPGNNLTK 133

RESULT 27
Q96K47 PRELIMINARY; PRT; 594 AA.
AC Q96K47;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ14701.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027607; BAB55229.1; -.
DR GO; GO:000507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
KW Hypothetical protein.
SQ SEQUENCE 594 AA; 65957 MW; C3EA02EDFBC58B38 CRC64;

Query Match 61.3%; Score 38; DB 4; Length 594;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
Db 302 CKPGNNLTK 310

RESULT 28
Q7UYT4 PRELIMINARY; PRT; 654 AA.
AC Q7UYT4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to peptidase.
GN RB393.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
```


RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294133; CAD71557.1; --
 KW Complete proteome.
 SQ SEQUENCE 654 AA; 70834 MW; 2BC43E15FAD6AD87 CRC64;

Query Match 61.3%; Score 38; DB 16; Length 654;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGQELTKQ 11
 |||||
 Db 446 PGQNLVKQ 454

RESULT 29

Q8IWF8 PRELIMINARY; PRT; 753 AA.
 AC Q8IWF8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to hypothetical protein FLJ12892.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (NCV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040285; AAH40285.1; --
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000923; BlueCu 1.
 DR PROSITE; PS00196; COPPER_BLUE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 753 AA; 83595 MW; 882A6B248030480C CRC64;

Query Match 61.3%; Score 38; DB 4; Length 753;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
 |||||
 Db 461 CKPGNNLT 469

RESULT 30

Q94H84 PRELIMINARY; PRT; 780 AA.
 AC Q94H84;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R.; Yuan Q.; Ouyang S.; Moffat K.S.; Hill J.N.; Gansberger K.;
 RA Brenner M.; Burgess S.; Hance M.; Shvartsbeyn M.; Tsitrin T.;
 RA Riggs F.; Hsiao J.; Zismann V.; Blunt S.; Pai G.; VanAken S.E.;
 RA Utterback T.R.; Feldblyum T.V.; Quackenbush J.; Salzberg S.L.;
 RA White O.; Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNBa0090P23 genomic sequence.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC084380; AAK52142.1; --
 DR Gramene; Q94H84; --
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000270; OPR PB1.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00564; PB1; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00666; PB1; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 780 AA; 87258 MW; 6D4BB12E04F15F1E CRC64;

Query Match 61.3%; Score 38; DB 10; Length 780;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQLTKQ 10
 |||||
 Db 178 RPQELKKQ 186

RESULT 31

Q7Z3N3 PRELIMINARY; PRT; 793 AA.
 AC Q7Z3N3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein DKFZp686G1990.
 GN DKFZP686G1990.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human retina;
 RA Lauber J.; Bahr A.; Mewes H.W.; Weil B.; Amid C.; Osanger A.; Fobo G.;
 RA Han M.; Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537652; CAD97804.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 793 AA; 88258 MW; AB0404EF5FAB5A39 CRC64;

Query Match 61.3%; Score 38; DB 4; Length 793;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
 |||||
 Db 501 CKPGNNLT 509

RESULT 32

Q9U5P6 PRELIMINARY; PRT; 978 AA.
 AC Q9U5P6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Microsomal aminopeptidase.
 GN H11-1.

OS Haemonchus contortus (Barber pole worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
OX NCBI_TaxID=6289;
RN [1]
RP SEQUENCE FROM N.A.
RA Graham M., Smith T.S., Munn E.A., Coadwell W.J., Newton S.E.,
RA Barker P.J.;
RT "Cloning and sequencing of variants of H11, the highly protective
RT membrane glycoprotein from Haemonchus contortus.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249941; CAB57357.1; -.
DR MEROPS; M01.015; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Aminopeptidase.
SQ SEQUENCE 978 AA; 112117 MW; D4615283D35AB8E7 CRC64;

Query Match 61.3%; Score 38; DB 5; Length 978;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELT 8
Db 788 CRPGQAT 795

RESULT 33
Q9JJS0 PRELIMINARY; PRT; 997 AA.
ID Q9JJS0
AC Q9JJS0; 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cegp1 protein.
GN CEGP1 OR CEGP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bahr A., Hankeln T., Winterpacht A., Zabel B., Schmidt E.R.;
RA "Comparative sequencing of Human chromosome 1p15 and mouse chromosome
RT 7.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AJ400878; CAB92293.1; -.
DR HSSP; P07204; 1ADX.
DR MGD; MGI:1928765; Cegf1.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 9.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 997 AA; 109923 MW; E0261CD9C8F70701 CRC64;

Query Match 61.3%; Score 38; DB 11; Length 997;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9
Db 198 CRPGFELAK 206

RESULT 34
Q9NQ36 PRELIMINARY; PRT; 999 AA.
ID Q9NQ36
AC Q9NQ36; 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CEGP1 protein.
GN CEGP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bahr A., Hankeln T., Winterpacht A., Zabel B., Schmidt E.R.;
RA "Comparative sequencing of Human chromosome 1p15 and mouse chromosome
RT 7.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AJ400877; CAB92285.1; -.
DR HSSP; P07204; 1ADX.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 7.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 999 AA; 109956 MW; 61334844A0053095 CRC64;

Query Match 61.3%; Score 38; DB 4; Length 999;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9
Db 200 CRPGFELAK 208

RESULT 35
Q9LPK1 PRELIMINARY; PRT; 1207 AA.
ID Q9LPK1
AC Q9LPK1; 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE F6N18.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,

RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F6N18 from chromosome
 I.",
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC017118; AAF25964.2; -;
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Peptidase_S8.
 DR InterPro; IPR001584; Rve.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 1.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00158; ZF_CCHC; 1.
 SQ SEQUENCE 1207 AA; 138738 MW; 60328FAB6B25A150 CRC64;

Query Match 61.3%; Score 38; DB 10; Length 1207;
 Best Local Similarity 77.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PGQELTKQG 11
 |||:||||
 DB 1001 PGQKLTKAG 1009

RESULT 36
 Q9C7Y1
 ID Q9C7Y1 PRELIMINARY; PRT; 1334 AA.
 AC Q9C7Y1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Copia-type polypeptide, putative.
 GN T9G5.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.",
 RL Nature 408:816-820(2000).
 DR EMBL; AC055769; AAG51247.1; -;
 DR PIR; E86451; E86451.

DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Peptidase_S8.
 DR InterPro; IPR001584; Rve.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 1.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00158; ZF_CCHC; 1.
 KW Polyprotein.
 SQ SEQUENCE 1334 AA; 153488 MW; A5718931BC7BD021 CRC64;

Query Match 61.3%; Score 38; DB 10; Length 1334;
 Best Local Similarity 77.8%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PGQELTKQG 11
 |||:||||
 DB 1096 PGQKLTKAG 1104

RESULT 37
 Q9FH39
 ID Q9FH39 PRELIMINARY; PRT; 1334 AA.
 AC Q9FH39;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Copia-type polypeptide.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katch T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 clones.",
 RT DNA Res. 7:31-63(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=21219200; PubMed=11319272;
 RA Terol J., Castillo M.C., Barques M., Perez-Alonso M., de Frutos R.;
 RT "Structural and evolutionary analysis of the copia-like elements in
 the Arabidopsis thaliana genome.",
 RL Mol. Biol. Evol. 18:882-892(2001).
 DR EMBL; AB022213; BAB11200.1; -;
 DR EMBL; AJ292423; CAC37622.1; -;
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Peptidase_S8.
 DR InterPro; IPR001584; Rve.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 1.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00158; ZF_CCHC; 1.
 KW Polyprotein.
 SQ SEQUENCE 1334 AA; 153430 MW; 49A18931BC7BD0AC CRC64;

Query Match 61.3%; Score 38; DB 10; Length 1334;
Best Local Similarity 77.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CRPGQELTKQ 11
|:|:|:|:|
Db 1096 PGQKLTAKG 1104

RESULT 38
Q8H3Z6 PRELIMINARY; PRT; 1335 AA.
ID Q8H3Z6
AC Q8H3Z6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P0597G07.2 protein.
GN P0597G07.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T.; Matsumoto T.; Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
clone:P0597G07."
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP004316; BAC16036.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR InterPro; IPR001357; BRCT.
DR Pfam; PF00533; BRCT; 3.
DR SMART; SM00292; BRCT; 4.
DR PROSITE; PS50172; BRCT; 3.
SQ SEQUENCE 1335 AA; 145373 MW; 2656CEB046F34B0D CRC64;

Query Match 61.3%; Score 38; DB 10; Length 1335;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
|:|:|:|:|
Db 1277 CKPGQSLNK 1285

RESULT 39
Q24406 PRELIMINARY; PRT; 110 AA.
ID Q24406
AC Q24406;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protamine.
GN MST35BB OR CG4478.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R;
RA Russell S.R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z46785; CAA86737.1; -.
DR PIR; S52158; S52158.
DR FlyBase; FBgn0013301; Mst35Bb.
SQ SEQUENCE 110 AA; 12329 MW; F77095E39F543B20 CRC64;

Query Match 59.7%; Score 37; DB 5; Length 110;

Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CRPGQELTKQ 11
|:|:|:|:|
Db 69 CAPSQKCSKQ 79

RESULT 40
Q24402 PRELIMINARY; PRT; 110 AA.
ID Q24402
AC Q24402;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protamine.
GN MST35BB OR CG4478.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R;
RA Russell S.R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z46784; CAA86736.1; -.
DR PIR; S52156; S52156.
DR FlyBase; FBgn0013301; Mst35Bb.
SQ SEQUENCE 110 AA; 12415 MW; B46395E39F4A1DFB CRC64;

Query Match 59.7%; Score 37; DB 5; Length 110;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11
|:|:|:|:|
Db 69 CAPSQKCSKQ 79

Search completed: May 5, 2004, 14:40:34
Job time : 4.76712 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:20 ; Search time 12.4144 Seconds
(without alignments)
568.992 Million cell updates/sec

Title: US-10-067-122B-2_COPY_133_157
Perfect score: 139
Sequence: 1 CRPWTNCSLDGRSVLKTGTTKDVV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	191	4	AAB66986 41bb prot
2	139	100.0	256	2	AAR64199 Murine 4-
3	139	100.0	256	2	AAR70978 4-1BB rec
4	139	100.0	256	2	AAW04173 Mouse rec
5	139	100.0	256	2	AAW26659 Mouse 4-1
6	139	100.0	256	2	AAW28687 Mouse Rec
7	139	100.0	256	2	AAW33215 Murine CD
8	139	100.0	256	5	AAE22581 Mouse rec
9	139	100.0	256	5	ABB75954 Murine cy
10	139	100.0	256	7	ADC25939 Murine re
11	139	100.0	256	7	ADe87549 Mouse rec
12	115	82.7	132	3	AAW94714 Tumour ne
13	115	82.7	219	2	AAW31759 A novel h
14	115	82.7	219	2	AAW92523 Human h4-
15	115	82.7	219	2	AAW92524 Human h4-
16	115	82.7	219	4	AAE08545 Human h4-
17	115	82.7	219	6	ABB84639 Human h4-
18	115	82.7	255	2	AAR74087 Human rec
19	115	82.7	255	2	AAR64197 Human 4-1
20	115	82.7	255	2	AAR70977 H4-1BB re
21	115	82.7	255	2	AAW26658 Human 4-1
22	115	82.7	255	2	AAW28688 Human rec
23	115	82.7	255	2	AAW33214 Human CD1
24	115	82.7	255	4	AAE08546 Human h4-
25	115	82.7	255	4	AAB50521 Human tum

Abb75955 Human cyt
Abr39863 Human MOC
Abb84640 Human h4-
Aae39531 Human pro
AGC78803 Human pro
Add25599 Binding d
AGE87541 Unknown h
Aaw04174 Human rec
Aay59508 OBM bindi
Adb17000 Murine RA
Aaw83200 Murine os
Aaw69958 Murine NF
Aaw68294 Murine NF
Aae08739 Murine re
Aay53649 A mouse r
Aay59509 OBM bindi
Aae04427 Murine re
Aae01994 Murine RA
Aae26104 Mouse RAN
Abp58179 Murine RA

26 115 82.7 255 5 ABB75955
27 115 82.7 255 6 ABR39863
28 115 82.7 255 6 ABB84640
29 115 82.7 255 7 AAE39531
30 115 82.7 255 7 ADC78803
31 115 82.7 255 7 ADD25599
32 115 82.7 255 7 ADE87541
33 102 73.4 255 2 AAW04174
34 86 61.9 201 3 AAY59508
35 86 61.9 443 7 ADB17000
36 86 61.9 625 2 AAW83200
37 86 61.9 625 2 AAW69958
38 86 61.9 625 2 AAW68294
39 86 61.9 625 2 AAE08739
40 86 61.9 625 3 AAY53649
41 86 61.9 625 3 AAY59509
42 86 61.9 625 4 AAE04427
43 86 61.9 625 4 AAE01994
44 86 61.9 625 5 AAE26104
45 86 61.9 625 6 ABP58179

ALIGNMENTS

RESULT 1
AAB66986
ID AAB66986 standard; protein; 191 AA.
XX
AC AAB66986;
XX
DT 19-APR-2001 (first entry)
XX
DE 41bb protein.
XX
KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
KW ischaemia; Parkinson's disease.
XX
OS Unidentified.
XX
PN WO200103719-A2.
XX
PD 18-JAN-2001.
XX
PF 07-JUL-2000; 2000WO-US018667.
XX
PR 09-JUL-1999; 99US-00350670.
PR 09-DEC-1999; 99US-00457647.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
XX
DR WPI; 2001-103031/11.
XX
PT Treating conditions leading to bone loss such as rheumatoid arthritis,
PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
PT protein in conjunction with e.g. inhibitors of interleukin and tumor
PT necrosis factor alpha.
XX
PS Disclosure; Fig 2; 316pp; English.
XX
CC The present invention relates to a method for treating conditions leading
CC to bone loss. The method comprises administering a purified and isolated
CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
CC in conjunction with other substances such as tumour necrosis factor-alpha
CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet

CC activating factor (PAF) antagonists. The method is useful for treating
CC conditions leading to bone loss such as rheumatoid arthritis, multiple
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
CC graft-versus-host disease (GVHD). Other diseases that can be treated
CC include acute pancreatitis, Alzheimer's disease, anorexia,
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
CC psoriasis and septic shock. The present sequence was used in a sequence
CC homology comparison
XX
SQ Sequence 191 AA;

Query Match 100.0%; Score 139; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 2
AAR64199
ID AAR64199 standard; protein; 256 AA.

XX AAR64199;
AC
XX
DT 25-MAR-2003 (revised)
DT 08-AUG-1995 (first entry)
XX
XX Murine 4-1BB polypeptide.
DE
XX T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
XX
OS Mus musculus.
XX
PN WO9426290-A1.
XX

PD 24-NOV-1994.
XX
XX 06-MAY-1994; 94WO-US005036.
XX
PR 07-MAY-1993; 93US-00060843.
XX
XX (IMMV) IMMUNEX CORP.
PA
XX Goodwin RG, Smith CA, Alderson MR;
PI
XX WPI; 1995-022265/03.
DR N-PSDB; AAQ75428.
XX

PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB
PT to transduce signal.
XX
PS Example 1; Page 44-45; 65pp; English.
XX

CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75422)
CC are useful in a pharmaceutical composition for stimulating the immune
CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring
CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.
CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation
CC of primary T-cells during the derivation of clonal T-cell lines. It may
CC also be used to stimulate proliferation of activated T-cells, used in
CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 3
AAR70978
ID AAR70978 standard; protein; 256 AA.

XX AAR70978;
AC
XX
DT 25-MAR-2003 (revised)
DT 16-OCT-1995 (first entry)
XX
XX 4-1BB receptor protein.
KW 4-1BB; receptor protein; immunosuppressive; autoimmune disease;
KW organ transplantation; cell membrane ligand.
XX
OS Mus sp.

XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
XX
PN WO9507984-A1.
XX
PD 23-MAR-1995.
XX
XX 15-SEP-1994; 94WO-US010457.
XX
PR 16-SEP-1993; 93US-00122796.
XX
XX (INDV) UNIV INDIANA FOUND.
PA
XX Kwon BS;
PI
XX WPI; 1995-131352/17.
DR N-PSDB; AAQ86127.
XX

PT Novel cDNA encoding human receptor protein H4-1BB - useful to produce the
PT protein which is used to treat autoimmune disease and facilitate organ
PT transplantation.
XX
PS Disclosure; Fig 1; 36pp; English.
XX
CC cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was
CC isolated using PCR primers based on the homologous mouse 4-1BB gene
CC (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR
CC -2003 to correct PN field.)
XX
SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 4
AAW04173
ID AAW04173 standard; protein; 256 AA.

XX AAW04173;
AC
XX
DT 12-DEC-1996 (first entry)
XX
DE Mouse receptor 4-1BB.
XX

KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW immunostimulant; cancer; autoimmune disease; graft rejection; therapy.
XX
OS Mus sp.
XX
XX WO9629348-A1.
XX
XX PD 26-SEP-1996.
XX
XX PF 22-MAR-1996; 96WO-US003965.
XX
XX PR 23-MAR-1995; 95US-00409851.
XX
XX PA (INDV) UNIV INDIANA FOUND.
XX
XX PI Kwon BS, Kang C;
XX
XX DR WPI; 1996-443138/44.
XX
XX DR N-PSDB; AAT39541.
XX
XX PT Monoclonal antibody specific for human receptor protein 4-1BB - used to
XX enhance proliferation and activation of T-cells for treatment of cancer
XX and to inhibit specific ligand binding for treating autoimmune diseases.
XX
XX PS Disclosure; Page 32-34; 48pp; English.
XX
XX CC Novel murine receptor protein 4-1BB (AAW04173) has the potential to
XX function as an accessory signaling molecule during T-cell activation and
XX proliferation. It may represent a cell surface molecule involved in T-
XX cell-APC interactions and may also act as a B-cell costimulator. It is
XX structurally related to members of the nerve growth factor receptor
XX superfamily. Its amino acid sequence was deduced from an isolated cDNA
XX clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was
XX identified and used to raise a monoclonal antibody useful in cancer and
XX autoimmune disease therapy
XX
XX SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 5
AAW26659
ID AAW26659 standard; protein; 256 AA.
XX
AC AAW26659;
XX
DT 25-MAR-2003 (revised)
DT 25-FEB-1998 (first entry)
XX
DE Mouse 4-1BB receptor.
XX
KW 4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell;
KW proliferation; immunostimulant.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX /label= Sig_peptide
XX
XX US5674704-A.
XX
XX PD 07-OCT-1997.
XX
XX PF 06-MAY-1994; 94US-00236918.
XX

PR 07-MAY-1993; 93US-00060843.
XX
XX PA (IMMV) IMMUNEX CORP.
XX
XX PI Alderson MR, Goodwin RG, Smith CA;
XX
XX DR WPI; 1997-502333/46.
XX
XX DR N-PSDB; AAT91027.
XX
XX PT DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell
XX proliferation in vitro, and as research tools.
XX
XX PS Disclosure; Col 39-40; 32pp; English.
XX
XX CC This protein comprises mouse 4-1BB, a member of the tumour necrosis
XX factor receptor superfamily that is expressed on helper, suppressor and
XX cytolytic T cells, as well as on mouse brain tissue. A novel claimed
XX cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned
XX and sequenced (see AAW26656) that binds to murine 4-1BB. 4-1BB-L,
XX especially its soluble extracellular domain, can be used to stimulate T-
XX cell proliferation in vitro, as a research tool and as an affinity ligand
XX for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 6
AAW28687
ID AAY28687 standard; protein; 256 AA.
XX
AC AAY28687;
XX
DT 13-OCT-1999 (first entry)
XX
DE Mouse Receptor 4-1BB protein.
XX
KW Mouse Receptor 4-1BB cDNA; Mouse Receptor 4-1BB protein; H4-1BB protein;
KW human 4-1BB protein; T cell activation; proliferation; immune response;
KW receptor protein; autoimmune disease; organ transplantation;
KW cancerous tumour; nerve growth factor receptor.
XX
OS Mus musculus.
XX
XX WO9936093-A1.
XX
XX PD 22-JUL-1999.
XX
XX PF 14-JAN-1999; 99WO-US000823.
XX
XX PR 14-JAN-1998; 98US-00007097.
XX
XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX PA (KWON/) KWON B S.
XX
XX PI Kwon BS;
XX
XX DR WPI; 1999-444325/37.
XX DR N-PSDB; AAX90763.
XX
XX PT Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
XX Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.
XX
XX PS Disclosure; Page 75; 86pp; English.
XX
XX CC The present sequence is mouse 4-1BB receptor protein. This protein has

CC 65% homology with human receptor protein 4-1BB. The protein has a
 CC putative leader sequence, a potential membrane anchor segment and other
 CC features of known receptor proteins. 4-1BB is structurally related to
 CC members of the nerve growth factor receptor. Probes derived from mouse 4-
 CC 1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its
 CC ligands, and various monoclonal antibodies have therapeutic uses. They
 CC may be used to enhance or suppress T cell activation and proliferation;
 CC for activation or inhibition of immune response; to block H4-1BB ligand
 CC binding; treating cancerous tumours and autoimmune diseases; and during
 CC organ transplantation

XX SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 |||||
 Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 7

AAAY33215
 ID AAY33215 standard; protein; 256 AA.

XX AC AAY33215;

XX DT 18-NOV-1999 (first entry)

XX DE Murine CD137 protein.

XX KW CD137; monocyte growth factor; proliferation; peripheral monocyte;
 KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;
 KW immunostimulatory; non-specific immune response; phagocytosis;
 KW intracellular destruction; microorganism; immune complex; antibody;
 KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
 KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
 KW bacterial; viral infection; immunosuppressant; gene therapy; murine.

XX OS Mus sp.

XX PN WO9944629-A2.

XX PD 10-SEP-1999.

XX PF 05-MAR-1999; 99WO-EP001440.

XX PR 05-MAR-1998; 98EP-00103859.

XX PA (MERC) MERCKLE GMBH.

XX PI Schwarz H, Langstein J;

XX DR WPI; 1999-550983/46.

XX PT Use of monocyte growth factor CD137 for stimulating proliferation of
 PT peripheral monocytes, particularly for treating immune deficiency, e.g.
 PT following cancer therapy.

XX PS Disclosure; Fig 1B; 57pp; German.

XX CC This invention describes a novel use of the human monocyte growth factor
 CC CD137, or its functional analogs, for (i) stimulating proliferation of
 CC peripheral monocytes; and (ii) treating diseases that are associated with
 CC disorders of a cellular system that includes monocytes (and/or their
 CC derived cells, precursor or progenitors) or where the origin and/or
 CC progression is treatable by stimulating proliferation of such cells. The
 CC products of the invention have antitumor, antibacterial, antiviral,
 CC antifungal and immunostimulatory activity. Stimulating proliferation of
 CC monocytes promotes the non-specific immune response, i.e. it increases
 CC phagocytosis and intracellular destruction of microorganisms, immune
 CC complexes and damaged cells, and improves antibody (in)dependent

CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
 CC diseases associated with a defective immune response where caused by
 CC inadequate numbers of active monocytes/macrophages, especially damage to
 CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation
 CC therapy; disorders of wound healing (e.g. in dialysis or diabetic
 CC patients, or those with chronic venous insufficiency); tumors; bacterial,
 CC fungal or viral infections; (non-)congenital or (non-)inherited diseases
 CC or injury to the immune system; injury induced by treatment with
 CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune
 CC disease, or transplant patients). Nucleic acid encoding (I) can be used
 CC similarly, in gene therapy procedures. Proliferation of peripheral
 CC monocytes is achieved independently of hematopoietic stem cells. This
 CC sequence represents the murine CD137 protein described in the method of
 CC the invention

XX SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 |||||
 Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 8

AAE22581

ID AAE22581 standard; protein; 256 AA.

XX AC AAE22581;

XX DT 26-JUL-2002 (first entry)

XX DE Mouse receptore 4-1BB protein.

XX KW Mouse; lymphokine; L2G25B; macrophage inflammatory protein 1 alpha;
 KW MIP-1alpha; immune disease; myeloid progenitor cell differentiation;
 KW 4-1BB; receptor.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Peptide 1..22

FT Protein /label= Signal_peptide

FT Modified-site /note= "Mature receptor 4-1BB protein"

FT Modified-site 128..130

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site 138..140

FT Modified-site /note= "Asn is N-glycosylated"

XX PN US6355476-B1.

XX PD 12-MAR-2002.

XX PF 30-JUL-1992; 92US-00922996.

XX PR 07-NOV-1988; 88US-00267577.

XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INC.

XX PI Kwon BS, Broxmeyer HE;

XX DR WPI; 2002-370577/40.

XX DR N-PSDB; AAD35694.

XX PT New isolated and purified cDNA designated L25G25B encoding the mouse
 PT lymphokine macrophage inflammatory protein 1 alpha which can be used for
 PT modulating early myeloid progenitor cell differentiation.

XX PS Disclosure; Fig 3; 81pp; English.

CC The invention relates to an isolated and purified cDNA containing mouse
CC lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage
CC inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by
CC which the immune cells communicate with each other. Lymphokines are used
CC therapeutically against immunologic diseases. Mouse lymphokine MIP-1alpha
CC can be used to modulate early myeloid progenitor cell differentiation.
CC The present sequence is mouse lymphokine receptor 4-1BB protein
XX
SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 9
ABB75954
ID ABB75954 standard; protein; 256 AA.

AC ABB75954;

DT 12-JUL-2002 (first entry)

DE Murine cytokine receptor 4-1BB.

XX Cytokine; receptor; 4-1BB; mouse.

OS Mus sp.

FH Key Location/Qualifiers
Peptide 1..23
FT /label= Signal_peptide
FT 24..256
FT /label= Mature_protein

XX US6355779-B1.

XX 12-MAR-2002.

PF 10-SEP-1998; 98US-00150864.

XX 07-MAY-1993; 93US-00060843.

PR 06-MAY-1994; 94US-00236918.

PR 05-AUG-1997; 97US-00910449.

XX (IMMV) IMMUNEX CORP.

XX Goodwin RG, Smith CA, Alderson MR;

XX WPI; 2002-380940/41.

DR N-PSDB; ABL54047.

XX New antibody specific for the cytokine 4-1BB-ligand, useful for
PT immunoaffinity purification of the ligand.

XX Example 1; Col 39-40; 31pp; English.

XX The present sequence is the protein sequence of the murine cytokine
CC receptor, 4-1BB. A portion of the extracellular (ligand binding) domain
CC of the receptor was utilised in a murine 4-1BB/human IgG1.Fc fusion
CC protein, which was used to identify the murine 4-1BB ligand (4-1BB-L, see
CC ABB75952). The invention provides novel murine and human 4-1BB-L
CC polypeptides and human 4-1BB polypeptides, as well as DNA sequences
CC encoding them, recombinant expression vectors and host cells, and methods
CC for producing the novel polypeptides by cultivating the transformed host
CC cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from
CC their extracellular domains, have therapeutic value. Antibodies that are
CC immunoreactive with 4-1BB-L or human 4-1BB are claimed

SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 10
ADC25939
ID ADC25939 standard; protein; 256 AA.

XX ADC25939;

AC 18-DEC-2003 (first entry)

DE Murine receptor 4-1BB protein.

XX receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;
KW cancer; murine; mouse.

XX Mus musculus.

XX US2003100745-A1.

XX 29-MAY-2003.

PF 04-FEB-2002; 2002US-00067122.

XX 07-NOV-1988; 88US-00267577.

PR 30-JUL-1992; 92US-00922996.

PR 01-FEB-1993; 93US-00012269.

XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX Kwon BS;

XX WPI; 2003-678138/64.

DR N-PSDB; ADC25938.

XX New cDNA gene encoding receptor protein 4-1BB, useful for isolating
PT similar DNA sequences, and the encoded polypeptide and an antibody to it,
PT useful for identifying ligands, and for modulating immune cell activity.

XX Claim 7; Fig 2; 77pp; English.

XX The invention relates to a novel cDNA gene encoding receptor protein 4-
CC 1BB. The cDNA gene of the invention demonstrates immunostimulant
CC activities and may be useful as a probe to isolate DNA sequences encoding
CC for proteins similar to the receptor protein encoded by the DNA. The
CC protein, its fragments and derivatives may be useful as a probe to
CC isolate ligands to receptor protein 4-1BB, for stimulating proliferation
CC of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand
CC binding. The antibody may be useful for enhancing T-cell proliferation or
CC activation. Finally, the invention may be useful with respect to cancer
CC research. The current sequence is that of the murine receptor 4-1BB
CC protein of the invention.

XX Sequence 256 AA;

Query Match 100.0%; Score 139; DB 7; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 11

ADE87549
 ID ADE87549 standard; protein; 256 AA.
 XX
 AC ADE87549;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse receptor H4-1BB.
 XX
 KW immunosuppressive; H4-1BB ligand binding blocker; mouse;
 KW receptor protein; H4-1BB; B-cell proliferation stimulator;
 KW T-cell proliferation enhancer; immune system suppressor; transplantation;
 KW autoimmune disease.
 XX
 OS Mus sp.
 XX
 PN US2003082157-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 12-JUN-2002; 2002US-00170997.
 XX
 PR 07-NOV-1988; 88US-00267577.
 PR 30-JUL-1992; 92US-00922996.
 PR 01-FEB-1993; 93US-00012269.
 PR 05-JUN-1995; 95US-00460976.
 PR 22-OCT-1997; 97US-00955573.
 XX
 PA (KWON/) KWON B S.
 XX
 PI Kwon BS;
 XX
 DR WPI; 2003-576599/54.
 DR N-PSDB; ADE87548.
 XX
 PT New cDNA, or its encoded receptor protein H4-1BB, useful as probes to
 PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking
 PT H4-1BB ligand binding to facilitate organ transplantation or treat
 PT autoimmune diseases.
 XX
 PS Disclosure; Fig 1; 19pp; English.
 XX
 CC The invention describes a cDNA, which encodes for human receptor protein
 CC H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe
 CC to isolate DNA sequences encoding for proteins similar to the receptor
 CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or
 CC derivatives, is useful as a probe for identifying ligands to the receptor
 CC protein H4-1BB, or for stimulating the proliferation of B-cells
 CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are
 CC useful for enhancing T-cell proliferation of activation. The cDNA or
 CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand
 CC binding, which is particularly useful for suppressing the immune system
 CC during transplantation, or for treating autoimmune diseases. This is the
 CC amino acid sequence of mouse receptor H4-1BB.
 XX
 SQ Sequence 256 AA;
 Query Match 100.0%; Score 139; DB 7; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDW 25
 DB 133 CRPWTNCSLDGRSVLKTGTTEKDW 157
 RESULT 12
 AAY94714
 ID AAY94714 standard; protein; 132 AA.
 XX
 AC AAY94714;
 XX
 DT 29-JAN-2001 (first entry)

XX Tumour necrosis factor receptor (TNFR) domain of 4-1BB protein.
 DE
 XX Tumour necrosis factor-receptor related protein; TR2; human; cancer;
 KW chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
 KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
 KW severely combined immunodeficiency; apoptosis inhibition;
 KW Alzheimer's disease; Parkinson's disease; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200056405-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US0007521.
 XX
 PR 22-MAR-1999; 99US-0125683P.
 PR 26-MAR-1999; 99US-0126522P.
 PR 20-MAY-1999; 99US-0135169P.
 PR 06-AUG-1999; 99US-0147383P.
 XX
 PA (NIJJ/) NI J.
 PA (ROSE/) ROSEN C A.
 PA (GENTZ/) GENTZ R L.
 XX
 PI Ni J, Rosen CA, Gentz RL;
 XX
 DR WPI; 2000-594519/56.
 XX
 PT Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
 PT and its two splice variants, useful for treating arthritis or
 PT inflammation, cancer (such as follicular lymphomas) and immunodeficiency
 PT disorders.
 XX
 PS Disclosure; Fig 16; 373pp; English.
 XX
 CC This invention relates to an isolated nucleic acid molecule encoding a
 CC human tumor necrosis factor (TNF)-receptor related protein TR2. Included
 CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
 CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
 CC member of the TNFR superfamily. The invention includes a method for the
 CC treatment of arthritis or inflammation using an antibody directed against
 CC a fragment of the TR2 protein. TR2 its agonists, antagonists and
 CC antibodies exhibit cytostatic, dermatological, antineoplastic,
 CC immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
 CC antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
 CC cerebroprotective activity. The methods are useful for treating arthritis
 CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
 CC immunodeficiency or for enhancing an in vivo leukocyte response to an
 CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia, and
 CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 CC inflammatory myopathies) and immunodeficiency disorders (such as severely
 CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 CC disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
 CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 CC antagonists are useful for treating or preventing autoimmune diseases and
 CC inhibit the growth, progression and/or metastasis of cancers. They are
 CC also used to activate, differentiate or proliferate cancerous cells or
 CC tissues, and can be used to treat diseases associated with increased cell
 CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 CC as sources for generating antibodies, as molecular weight markers. This
 CC sequence represents the tumor necrosis factor receptor (TNFR) domain of
 CC the human 4-1BB protein. The sequence was used in the characterisation of
 CC the TR2 receptor protein of the invention
 XX
 SQ Sequence 132 AA;
 Query Match 82.7%; Score 115; DB 3; Length 132;
 Best Local Similarity 80.0%; Pred. No. 2.7e-09;

Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 106 CRPWTNCSLDGKSVLVNGTKERDVV 130

RESULT 13
AAW31759
ID AAW31759 standard; protein; 219 AA.
XX
AC AAW31759;
XX
DT 01-APR-1998 (first entry)
XX
DE A novel human h4-1BBSV receptor.
XX
KW h4-1BBSV receptor; 4-1BB receptor splicing variant; endotoxigenic shock;
KW tumour necrosis factor; TNF ligand; T-cell activation; inflammation;
KW tumour prevention; viral infection; autoimmune disease;
KW cellular proliferation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .18
FT Protein /note= "putative signal sequence"
FT Domain /note= "mature protein"
FT Domain /note= "soluble extracellular domain"
FT Domain /note= "transmembrane domain"
XX
PN WO9733898-A1.
XX
PD 18-SEP-1997.
XX
PF 15-MAR-1996; 96WO-US003587.
XX
PR 15-MAR-1996; 96WO-US003587.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz RL;
XX
DR WPI; 1997-470806/43.
DR N-PSDB; AAT88969.
XX
PT Human 4-1BB receptor splicing variant and related DNA - used to develop
PT products for treating e.g. tumours, viral infection, endotoxigenic shock,
PT autoimmune disease or bone resorption.
XX
PS Claim 15; Fig 1; 73pp; English.
XX
CC The present sequence represents a novel human h4-1BBSV receptor. This is
CC a human 4-1BB receptor splicing variant. The 4-1BB ligand is a member of
CC the tumour necrosis factor (TNF) family of ligands. It is induced by T-
CC cell activation. The h4-1BBSV receptor nucleic acid and protein can be
CC used for diagnosis and therapy. In particular, agonists of h4-1BBSV
CC receptor can be used to treat and/or prevent tumours, restenosis,
CC cytotoxicity, bacterial and viral infection, deleterious effects of
CC ionising radiation, autoimmune disease, AIDS and graft-host rejection, to
CC regulate immune responses, wound healing and cellular proliferation.
CC Antagonists can be used to treat and/or prevent endotoxigenic shock,
CC inflammation, cerebral malaria, activation of the HIV virus, graft
CC rejection, bone resorption and cachexia
XX
SQ Sequence 219 AA;

Query Match 82.7%; Score 115; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 5e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 97 CRPWTNCSLDGKSVLVNGTKERDVV 121

RESULT 14
AAW92523
ID AAW92523 standard; protein; 219 AA.
XX
AC AAW92523;
XX
DT 23-APR-1999 (first entry)
XX
DE Human h4-1BBSV receptor protein.
XX
KW h4-1BBSV receptor; human; splice variant; antagonist; treatment;
KW disease prevention; endotoxigenic shock; inflammation; cerebral malaria;
KW HIV virus activation; graft rejection; bone resorption; cachexia;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .18
FT Protein /label= signal_peptide
FT Protein 19. .219
XX
PN US5874240-A.
XX
PD 23-FEB-1999.
XX
PF 13-MAR-1997; 97US-00816605.
XX
PR 15-MAR-1996; 96US-0013474P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Dillon PJ, Yu G, Ni J, Gentz R;
XX
DR WPI; 1999-179974/15.
DR N-PSDB; AAX02162.
XX
PT New nucleic acid encoding human 4-1BB receptor splicing variant - useful
PT in treating h4-1BBSV mediated disease states such as endotoxigenic shock,
PT inflammation, graft rejection and inactivation of HIV.
XX
PS Claim 1a; Fig 1A-B; 28pp; English.
XX
CC This sequence represents a novel human h4-1BBSV receptor protein which is
CC used in a method for making a human 4-1BB receptor splice variant which
CC acts as an antagonist. The antagonist polypeptides may be used to
CC treat/prevent disease states mediated by h4-1BBSV receptors such as
CC endotoxigenic shock, inflammation, cerebral malaria, activation of the HIV
CC virus, graft rejection, bone resorption and cachexia. The h4-1BBSV coding
CC sequences are useful in gene therapy
XX
SQ Sequence 219 AA;

Query Match 82.7%; Score 115; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 5e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 97 CRPWTNCSLDGKSVLVNGTKERDVV 121

RESULT 15
AAW92524
ID AAW92524 standard; protein; 219 AA.
XX
AC AAW92524;

XX
DT 23-APR-1999 (first entry)
XX
DE Human h4-1BBSV receptor protein variant.
XX
KW h4-1BBSV receptor; human; splice variant; antagonist; treatment;
KW disease prevention; endotoxin shock; inflammation; cerebral malaria;
KW HIV virus activation; graft rejection; bone resorption; cachexia;
KW gene therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 33..34
FT /note= "Site of deletion of residues GTFCDNRRNQICSPC
FT PPNFSSAGGQRTCDICRQCK corresponding to amino acid
FT residues 34-69 of the wild-type protein"
XX
PN US5874240-A.
XX
PD 23-FEB-1999.
XX
PF 13-MAR-1997; 97US-00816605.
XX
PR 15-MAR-1996; 96US-0013474P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Dillon PJ, Yu G, Ni J, Gentz R;
XX WPI; 1999-179974/15.
XX
PT New nucleic acid encoding human 4-1BB receptor splicing variant - useful
PT in treating h4-1BBSV mediated disease states such as endotoxin shock,
PT inflammation, graft rejection and inactivation of HIV.
XX
PS Claim 29; Page; 28pp; English.
XX
CC This sequence represents a human h4-1BBSV receptor protein variant which
CC has antagonistic properties. This protein may be used to treat/prevent
CC disease states mediated by h4-1BBSV receptors such as endotoxin shock,
CC inflammation, cerebral malaria, activation of the HIV virus, graft
CC rejection, bone resorption and cachexia. The h4-1BBSV coding sequences
CC are useful in gene therapy. This sequence does not appear in the
CC specification but has been created from the wild-type sequence
CC represented in Fig 2
XX
SQ Sequence 219 AA;

Query Match 82.7%; Score 115; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 5e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 97 CRPWTNCSLDGRSVLKTGTTEKDVV 121

RESULT 16
AAE08545
ID AAE08545 standard; protein; 219 AA.
XX
AC AAE08545;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human h4-1BB splicing variant (h4-1BBSV) receptor.
XX
KW Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;
KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;
KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;
KW AIDS; Graft-host rejection; cellular proliferation; cerebral malaria;

KW bone resorption; human immunodeficiency virus; HIV; graft rejection;
KW inflammation; antibacterial; immunosuppressive; vulnary; vasotropic;
KW antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= Signal_peptide
FT Protein 19..219
FT /label= Mature_human_h4-1BBSV_receptor
FT Domain 19..150
FT /label= Extracellular_domain
FT Domain 151..177
FT /label= Transmembrane_domain
XX US2001014465-A1.
XX 16-AUG-2001.
XX 19-DEC-2000; 2000US-00739394.
XX 15-MAR-1996; 96US-0013474P.
PR 13-MAR-1997; 97US-00816605.
PR 22-FEB-1999; 99US-00253549.
XX
PA (NIJJ/) NI J.
PA (YUGG/) YU G.
PA (GENT/) GENTZ R.
PA (DILL/) DILLON P J.
XX
PI Ni J, Yu G, Gentz R, Dillon PJ;
XX
DR WPI; 2001-529104/58.
DR N-PSDB; AAD15246.
XX
PT New human 4-1BB receptor splicing variant polypeptides and
PT polynucleotides, useful for research, diagnosis, prevention and treatment
PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
PT syndrome and graft rejection.
XX
PS Claim 15; Fig 1; 28pp; English.
XX
CC The present invention relates to an isolated human 4-1BB receptor
CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
CC gene therapy. h4-1BBSV is useful for research, biological, clinical and
CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives
CC are useful as an immunogen to produce antibodies which are useful for
CC isolating and identifying clones expressing the polypeptide or to purify
CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of
CC disorders of cells, tissues and organisms and its nucleic acid is useful
CC for detecting complementary polynucleotides for e.g. as a diagnostic
CC reagent and for chromosomal identification. h4-1BBSV receptor agonists
CC are useful for preventing, treating tumours, restenosis, cytotoxicity,
CC bacterial and viral infection, deleterious effects of ionising radiation,
CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-
CC host rejection, to regulate immune responses, wound healing and cellular
CC proliferation and antagonists are useful for treating and/or preventing
CC endotoxin shock, inflammation, cerebral malaria, activation of human
CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
CC cachexia. The present sequence is human h4-1BBSV receptor
XX
SQ Sequence 219 AA;

Query Match 82.7%; Score 115; DB 4; Length 219;
Best Local Similarity 80.0%; Pred. No. 5e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 97 CRPWTNCSLDGRSVLKTGTTEKDVV 121

RESULT 17
ABB84639
ID ABB84639 standard; protein; 219 AA.
XX
AC ABB84639;
XX
XX
DT 05-FEB-2003 (first entry)
XX
DE Human h4-1BBSV receptor.
XX
KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;
KW anti-HIV; antibacterial; anti-inflammatory; protozoacide; immunomodulator;
KW vasotropic; gene therapy; chromosome mapping; extracellular domain;
KW endotoxigenic shock; cytotoxicity; cerebral malaria; autoimmune disease;
KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;
KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;
KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;
KW autoimmune disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .18
FT Protein 19. .219
FT /label= h4-1BBSV_receptor
FT /note= "region specifically claimed in claim 1b"
FT Domain 19. .150
FT /label= soluble_extracellular_domain
FT /note= "region specifically claimed in claim 1a"
FT Domain 151. .177
FT /label= transmembrane_domain
XX
XX
PN US2002127651-A1.
XX
PD 12-SEP-2002.
XX
PF 15-MAR-2002; 2002US-00097330.
XX
PR 15-MAR-1996; 96US-0013474P.
PR 13-MAR-1997; 97US-00816605.
PR 22-FEB-1999; 99US-00253549.
PR 19-DEC-2000; 2000US-00739394.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz RL, Dillon PJ;
XX
XX WPI; 2003-066900/06.
DR N-PSDB; ABS57520.
XX
XX Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,
PT providing resistance to bacteria, viruses and parasites, to induce
PT proliferation of endothelial cells, and to treat restenosis.
XX
XX Example 2; Fig 1A-B; 29pp; English.
PS
XX This invention describes a novel human h4-1BBSV receptor or a sequence
CC that is at least 85% identical to the h4-1BBSV receptor. The product of
CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,
CC antibacterial, anti-inflammatory, protozoacide, immunomodulator and
CC vasotropic activity and can be used for gene therapy and chromosome
CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to
CC a disease related to underexpression of h4-1BBSV or for identifying
CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV
CC receptor polypeptide is useful for treating and/or preventing endotoxigenic
CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human
CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or
CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired
CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,
CC viruses and parasites, to induce proliferation of endothelial cells and
CC certain haematopoietic cells, to treat restenosis and to prevent certain

CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.
CC This sequence represents the human h4-1BBSV receptor described in the
CC disclosure of the invention
XX
SQ Sequence 219 AA;
Query Match 82.7%; Score 115; DB 6; Length 219;
Best Local Similarity 80.0%; Pred. No. 5e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB 97 CRPWTNCSLDGKSVLVNGTKERDVV 121
RESULT 18
AAR74087
ID AAR74087 standard; protein; 255 AA.
XX
AC AAR74087;
XX
DT 21-JAN-1996 (first entry)
XX
DE Human receptor induced by lymphocyte activation (ILA).
XX
KW ILA; receptor inducible by lymphocyte activation; disease diagnosis;
KW antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .17
FT /note= "signal peptide"
FT Misc-difference 138
FT /note= "potential N-glycosylation site"
FT Misc-difference 149
FT /note= "potential N-glycosylation site"
FT Domain 187. .213
FT /note= "transmembrane domain"
FT Misc-difference 234
FT /note= "casein-kinase-II phosphorylation site"
FT Misc-difference 235
FT /note= "casein-kinase-II phosphorylation site"
FT Binding-site 241. .244
FT /note= "potential ligand binding site"
FT Misc-difference 242
FT /note= "protein-kinase phosphorylation site"
XX
PN CA2108401-A.
XX
XX 28-MAR-1995.
PD
XX 14-OCT-1993; 93CA-02108401.
PF
XX 27-SEP-1993; 93US-00127693.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Lotz M, Schwarz H;
PI
XX WPI; 1995-194420/26.
DR
XX N-PSDB; AAR74087.
XX
XX New receptor inducible by lymphocyte activation - used to develop prods.
PT for the diagnosis and treatment of inflammatory host defence pathology.
XX
XX Claim 55; Page 61; 91pp; English.
PS
XX ILA may be used to identify a host defence inflammatory response in body
CC tissue. The ILA agents can be used to detect an ILA-mediated pathology
CC such as atherosclerosis, autoimmune disease (rheumatoid arthritis,
CC transplant rejection, pathogenic host defence responses to microorganism
CC and malignancy such as lung carcinoma

```
XX SQ Sequence 255 AA;
Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 19
AAR64197
ID AAR64197 standard; protein; 255 AA.
XX AC AAR64197;
XX DT 25-MAR-2003 (revised)
XX DT 08-AUG-1995 (first entry)
XX DE Human 4-1BB polypeptide.
XX KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
XX KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
XX OS Homo sapiens.
XX PN WO9426290-A1.
XX PD 24-NOV-1994.
XX PF 06-MAY-1994; 94WO-US005036.
XX PR 07-MAY-1993; 93US-00060843.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Goodwin RG, Smith CA, Alderson MR;
XX DR WPI; 1995-022265/03.
XX DR N-PSDB; AAQ75424.
XX FT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB
XX PT to transduce signal.
XX PS Claim 39; Page 47-48; 65pp; English.
XX CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75423)
XX CC are useful in a pharmaceutical composition for stimulating the immune
XX CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring
XX CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.
XX CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation
XX CC of primary T-cells during the derivation of clonal T-cell lines. It may
XX CC also be used to stimulate proliferation of activated T-cells, used in
XX CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 20
AAR70977
ID AAR70977 standard; protein; 255 AA.
XX AC AAR70977;
```

```
XX 25-MAR-2003 (revised)
DT 16-OCT-1995 (first entry)
XX H4-1BB receptor protein.
DE H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
KW organ transplantation; cell membrane ligand.
XX OS Homo sapiens.
XX PN WO9507984-A1.
XX PD 23-MAR-1995.
XX PF 15-SEP-1994; 94WO-US010457.
XX PR 16-SEP-1993; 93US-00122796.
XX PA (INDV ) UNIV INDIANA FOUND.
XX PI Kwon BS;
XX DR WPI; 1995-131352/17.
XX DR N-PSDB; AAQ86126.
XX PT Novel cDNA encoding human receptor protein H4-1BB - useful to produce the
XX PT protein which is used to treat auto-immune disease and facilitate organ
XX PS transplantation.
XX PS Claim 6; Fig 2; 36pp; English.
XX CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using
XX CC probes based on the mouse receptor protein 4-1BB gene. The PCR product
XX CC was used to screen a cDNA library of activated human T-cells. The
XX CC isolated cDNA (AAQ86126), deposited as NRRL AAB21131, encoded the human
XX CC homolog, H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct
XX CC PN field.)
XX SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 21
AAW26658
ID AAW26658 standard; protein; 255 AA.
XX AC AAW26658;
XX DT 25-MAR-2003 (revised)
XX DT 25-FEB-1998 (first entry)
XX DE Human 4-1BB receptor.
XX KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte; T cell;
XX KW proliferation; immunostimulant.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT Peptide 1..23
XX FT Domain 24..186
XX FT Modified-site 115..117
XX FT /note= "Asn is N-glycosylated"
```


FT Modified-site 126..128 /note= "Asn is N-glycosylated"
FT Domain 187..213 /label= Transmembrane
FT Domain 214..255 /label= Extracellular
XX US5674704-A.
XX 07-OCT-1997.
XX 06-MAY-1994; 94US-00236918.
XX 07-MAY-1993; 93US-00060843.
XX (IMMV) IMMUNEX CORP.
XX Alderson MR, Goodwin RG, Smith CA;
XX WPI; 1997-502333/46.
XX N-PSDB; AAT91026.
XX DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell proliferation in vitro, and as research tools.
XX Example 2; Col 43-44; 32pp; English.
XX This protein comprises human 4-1BB, a member of the tumour necrosis factor receptor superfamily that is expressed on cells that include, but are not limited to, stimulated human peripheral blood lymphocytes. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT91026) obtained from human peripheral blood T-lymphocytes. A novel claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned and sequenced (see AAW26657) that binds to 4-1BB. 4-1BB-L, especially its soluble extracellular domain, can be used to stimulate T-cell proliferation in vitro, as a research tool and as an affinity ligand for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 255 AA;
SQ Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157
RESULT 22
AAV28688
ID AAY28688 standard; protein; 255 AA.
XX AAY28688;
XX 13-OCT-1999 (first entry)
XX Human receptor protein 4-1BB.
XX Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation; mouse 4-1BB cDNA; monoclonal antibody; immune response;
KW organ transplantation; autoimmune disease; diabetes; cancerous tumour;
KW rheumatoid arthritis; lupus; nerve growth factor receptor.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Protein 18..255
FT /note= "Purified human 4-1BB"
XX WO9936093-A1.
XX 22-JUL-1999.

XX 14-JAN-1999; 99WO-US000823.
XX 14-JAN-1998; 98US-00007097.
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA (KWON/) KWON B S.
XX Kwon BS;
PI WPI; 1999-444325/37.
XX N-PSDB; AAZ08961.
XX Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.
XX Claim 4; Page 77-78; 86pp; English.
XX The present sequence is a human receptor protein 4-1BB. 4-1BB is structurally related to members of the nerve growth factor receptor. It contains a putative zinc finger structure similar to that of yeast eIF-2b protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of 4-1BB. The H4-1BB protein, its ligands, and various monoclonal antibodies have therapeutic uses. They may be used to enhance or suppress T cell activation and proliferation; B cell proliferation; treating cancerous tumours and AIDS. The use of H4-1BB to block H4-1BB ligand binding has practical application in the suppression of immune system during organ transplantation or against autoimmune diseases including diabetes, rheumatoid arthritis, and lupus
XX Sequence 255 AA;
SQ Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157
RESULT 23
AAV33214
ID AAY33214 standard; protein; 255 AA.
XX AAY33214;
XX 18-NOV-1999 (first entry)
XX Human CD137 protein.
XX CD137; monocyte growth factor; proliferation; peripheral monocyte; treatment; disease; antitumor; antibacterial; antiviral; antifungal;
KW immunostimulatory; non-specific immune response; phagocytosis;
KW intracellular destruction; microorganism; immune complex; antibody;
KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal; bacterial; viral infection; immunosuppressant; gene therapy; human.
XX Homo sapiens.
XX WO9944629-A2.
XX 10-SEP-1999.
XX 05-MAR-1999; 99WO-EP001440.
XX 05-MAR-1998; 98EP-00103859.
XX (MERC) MERCKLE GMBH.
XX Schwarz H, Langstein J;
XX

DR WPI; 1999-550983/46.
XX N-PSDB; AAZ09769.
PT Use of monocyte growth factor CD137 for stimulating proliferation of
PT peripheral monocytes, particularly for treating immune deficiency, e.g.
PT following cancer therapy.
XX
XX
PS Claim 12; Fig 1A; 57pp; German.
XX
XX This invention describes a novel use of the human monocyte growth factor
CC CD137, or its functional analogs, for (i) stimulating proliferation of
CC peripheral monocytes; and (ii) treating diseases that are associated with
CC disorders of a cellular system that includes monocytes (and/or their
CC derived cells, precursor or progenitors) or where the origin and/or
CC progression is treatable by stimulating proliferation of such cells. The
CC products of the invention have antitumor, antibacterial, antiviral,
CC antifungal and immunostimulatory activity. Stimulating proliferation of
CC monocytes promotes the non-specific immune response, i.e. it increases
CC phagocytosis and intracellular destruction of microorganisms, immune
CC complexes and damaged cells, and improves antibody (in)dependent
CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
CC diseases associated with a defective immune response where caused by
CC inadequate numbers of active monocytes/macrophages, especially damage to
CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation
CC therapy; disorders of wound healing (e.g. in dialysis or diabetic
CC patients, or those with chronic venous insufficiency); tumors; bacterial,
CC fungal or viral infections; (non-)congenital or (non-)inherited diseases
CC or injury to the immune system; injury induced by treatment with
CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune
CC disease, or transplant patients). Nucleic acid encoding (I) can be used
CC similarly, in gene therapy procedures. Proliferation of peripheral
CC monocytes is achieved independently of hematopoietic stem cells. This
CC sequence represents the human CD137 protein described in the method of
CC the invention
XX
SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CRPWTNCSLDGSRVLKGTGTEKDWV 25
Db 133 CRPWTNCSLDGSKSVLVNGTKERDVV 157

RESULT 24
AAE08546
ID AAE08546 standard; protein; 255 AA.

XX AAE08546;
AC
XX
XX
DT 15-NOV-2001 (first entry)
XX
DE Human h4-1BB receptor.
XX
KW Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;
KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;
KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;
KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;
KW bone resorption; human immunodeficiency virus; HIV; graft rejection;
KW inflammation; antibacterial; immunosuppressive; vulnery; vasotropic;
KW antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.
XX
OS Homo sapiens.
XX
XX US2001014465-A1.
XX
XX 16-AUG-2001.
PD
XX
XX 19-DEC-2000; 2000US-00739394.
PF
XX
XX 15-MAR-1996; 96US-0013474P.
PR

PR 13-MAR-1997; 97US-00816605.
PR 22-FEB-1999; 99US-00253549.
XX
PA (NIJ/) NI J.
PA (YUGG/) YU G.
PA (GENT/) GENTZ R.
PA (DILL/) DILLON P J.
XX
PI Ni J, Yu G, Gentz R, Dillon PJ;
XX WPI; 2001-529104/58.
DR
XX
XX New human 4-1BB receptor splicing variant polypeptides and
PT polynucleotides, useful for research, diagnosis, prevention and treatment
PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
PT syndrome and graft rejection.
XX
PS Disclosure; Fig 2; 28pp; English.

XX The present invention relates to an isolated human 4-1BB receptor
CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
CC gene therapy. h4-1BBSV is useful for research, biological, clinical and
CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives
CC are useful as an immunogen to produce antibodies which are useful for
CC isolating and identifying clones expressing the polypeptide or to purify
CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of
CC disorders of cells, tissues and organisms and its nucleic acid is useful
CC for detecting complementary polynucleotides for e.g. as a diagnostic
CC reagent and for chromosomal identification. h4-1BBSV receptor agonists
CC are useful for preventing, treating tumours, restenosis, cytotoxicity,
CC bacterial and viral infection, deleterious effects of ionising radiation,
CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-
CC host rejection, to regulate immune responses, wound healing and cellular
CC proliferation and antagonists are useful for treating and/or preventing
CC endotoxin shock, inflammation, cerebral malaria, activation of human
CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
CC cachexia. The present sequence is human h4-1BB receptor
XX
SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGSRVLKGTGTEKDWV 25
Db 133 CRPWTNCSLDGSKSVLVNGTKERDVV 157

RESULT 25
AAB50521

ID AAB50521 standard; protein; 255 AA.

XX AAB50521;

XX
DT 15-MAR-2001 (first entry)

XX Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.

KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neutropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.

XX Homo sapiens.

XX WO200071150-A1.

XX

30-NOV-2000.
18-MAY-2000; 2000WO-US013515.
20-MAY-1999; 99US-0135164P.
(HUMA-) HUMAN GENOME SCI INC.
Wei Y, Ruben SM, Gentz RL, Ni J;
WPI; 2001-041051/05.
Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.
Disclosure; Fig 2; 285pp; English.
The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nontropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention
Sequence 255 AA;
Query Match 82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0
QY 1 CRPWTNCSLDGRSVLKGTGTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157
RESULT 26.
ABB75955
ID ABB75955 standard; protein; 255 AA.
AC ABB75955;
XX AC
XX AC
DT 12-JUL-2002 (first entry)
XX
DE Human cytokine receptor 4-1BB.
XX
KW Cytokine; receptor; 4-1BB; human.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH Key 1..23
FT Peptide /label= Signal_peptide
FT Protein 24..255
FT /label= Mature_protein
FT Domain 24..186
FT /note= "extracellular domain"

```

FT Modified-site 138. .140
FT /note= "Asn is N-glycosylated"
FT Modified-site 149. .151
FT /note= "Asn is N-glycosylated"
FT Region 186. .213
FT /note= "transmembrane region"
FT Domain 214. .255
FT /note= "cytoplasmic domain"
XX
PN US6355779-B1.
XX
XX 12-MAR-2002.
XX
XX 10-SEP-1998; 98US-00150864.
XX
XX 07-MAY-1993; 93US-00060843.
PR 06-MAY-1994; 94US-00236918.
PR 05-AUG-1997; 97US-00910449.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Goodwin RG, Smith CA, Alderson MR;
PI
XX WPI; 2002-380940/41.
DR N-PSDB; ABL54048.
DR
XX
XX New antibody specific for the cytokine 4-1BB-ligand, useful for
PT immunoaffinity purification of the ligand.
PT
XX
XX Example 2; Col 43-44; 31pp; English.
XX
CC The present sequence is the protein sequence of the human cytokine
CC receptor, 4-1BB. The sequence was deduced from a cDNA clone (see
CC ABL54048) obtained from a human peripheral blood T-lymphocyte cDNA
CC library. It shows 60% identity to murine 4-1BB (see ABB75954). A portion
CC of the extracellular (ligand binding) domain of the human 4-1BB cytokine
CC receptor was utilised in a human 4-1BB/human IgG1 Fc fusion protein,
CC which was used to identify the human 4-1BB ligand (4-1BB-L, see
CC ABB75953). The invention provides novel murine and human 4-1BB-L
CC polypeptides and human 4-1BB polypeptides, as well as DNA sequences
CC encoding them, recombinant expression vectors and host cells, and methods
CC for producing the novel polypeptides by cultivating the transformed host
CC cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from
CC their extracellular domains, have therapeutic value. Antibodies that are
CC immunoreactive with 4-1BB-L or human 4-1BB are claimed
XX
XX
SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 5; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 27
ABR39863
ID ABR39863 standard; protein; 255 AA.
XX
XX ABR39863;
XX
XX 11-AUG-2003 (first entry)
XX Human MOCEPTIN polypeptide.
XX
XX MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic;
KW antilipemic; antiarteriosclerotic; antidiabetic; cerebroprotective;
KW hypotensive; immunomodulator; antidepressant; human; receptor.
XX
XX Homo sapiens.
XX

```

FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein /note= "putative signal peptide"
FT Domain 18..255
FT Domain /note= "mature protein"
FT Domain 18..186
FT Domain /note= "extracellular domain"
FT Domain 187..213
FT Domain /note= "transmembrane domain"
FT Domain 214..255
FT Domain /note= "intracellular domain"
XX
PN WO2003011325-A1.
XX
PD 13-FEB-2003.
XX
XX
PF 25-JUL-2002; 2002WO-IB003499.
XX
PR 27-JUL-2001; 2001US-0308142P.
XX
PA (GEST) GENSET SA.
XX
PI Lucas J, Dialynas D, Briggs K;
XX
DR WPI; 2003-268084/26.
DR N-PSDB; ACC47324.
XX
XX New agonist and antagonist of MOCEPTIN (a member of the Tumor Necrosis
PT Factor Receptor family) activity, useful for preventing or treating
PT obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing
PT body mass.
XX
PS Disclosure; Page 32-33; 37pp; English.
XX
XX The invention relates to an agonist or antagonist of MOCEPTIN (a member
CC of the Tumour Necrosis Factor Receptor family) activity. The antagonist
CC or agonist of MOCEPTIN activity, or the composition comprising the
CC agonist or antagonist, is useful for preventing or treating an obesity-
CC related disorder or disease in an individual. In particular, the agonist
CC of MOCEPTIN activity is useful for treating or preventing obesity-related
CC diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance,
CC diabetes, stroke or hypertension. The agonist is also useful for reducing
CC body mass and maintaining weight loss. The antagonist of MOCEPTIN
CC activity is useful for increasing body mass, or for treating or
CC preventing disorders associated with excessive weight loss, e.g.
CC cachexia, cancer-related weight loss, AIDS-related weight loss, chronic
CC inflammatory disease-related weight loss, or anorexia. The present
CC sequence represents a human MOCEPTIN polypeptide
XX
SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 6; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 28
ABB84640
ID ABB84640 standard; protein; 255 AA.
XX
AC ABB84640;
XX
DT 05-FEB-2003 (first entry)
XX
DE Human h4-1BB receptor.
XX
KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;
KW anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator;
KW vasotrophic; gene therapy; chromosome mapping; extracellular domain;

KW endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease;
KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;
KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;
KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;
KW autoimmune disease; h4-1BB.
XX
OS Homo sapiens.
XX
PN US2002127651-A1.
XX
PD 12-SEP-2002.
XX
PF 15-MAR-2002; 2002US-00097330.
XX
PR 15-MAR-1996; 96US-0013474P.
PR 13-MAR-1997; 97US-00816605.
PR 22-FEB-1999; 99US-00253549.
PR 19-DEC-2000; 2000US-00739394.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz RL, Dillon PJ;
XX
DR WPI; 2003-066900/06.
XX
XX Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,
PT providing resistance to bacteria, viruses and parasites, to induce
PT proliferation of endothelial cells, and to treat restenosis.
XX
PS Disclosure; Fig 2; 29pp; English.
XX
XX This invention describes a novel human h4-1BBSV receptor or a sequence
CC that is at least 85% identical to the h4-1BBSV receptor. The product of
CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,
CC antibacterial, antiinflammatory, protozoacide, immunomodulator and
CC vasotropic activity and can be used for gene therapy and chromosome
CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to
CC a disease related to underexpression of h4-1BBSV or for identifying
CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV
CC receptor polypeptide is useful for treating and/or preventing endotoxic
CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human
CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or
CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired
CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,
CC viruses and parasites, to induce proliferation of endothelial cells and
CC certain haematopoietic cells, to treat restenosis and to prevent certain
CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.
CC This sequence represents the human 4-1BB receptor described in the
CC disclosure of the invention
XX
SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 6; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 29
AAE39531
ID AAE39531 standard; protein; 255 AA.
XX
AC AAE39531;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human protein SEQ ID NO: 2.
XX
KW Human; adhesive; packaging.
KW

OS	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FH	Misc-difference 107
FT	/note= "Encoded by AGA"
FT	
XX	
PN	US2003000851-A1.
XX	
PD	02-JAN-2003.
XX	
PF	08-JUN-2001; 2001US-00877336.
XX	
PR	08-JUN-2001; 2001US-00877336.
XX	
PA	(WALS/) WALSH J C.
PA	(HAWK/) HAWKINS K E.
XX	
PI	Walsh JC, Hawkins KE;
XX	
DR	WPI; 2003-266968/26.
DR	N-PSDB; AAD59981.
XX	
PT	Paper board container manufacture for soap boxes, involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction.
XX	
PS	Disclosure; Page 12-13; 46pp; English.
XX	
CC	The invention relates to a method and apparatus for applying adhesive to packaging in a variety of configurations. The method involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction. The invention is useful for e.g. soap boxes, cereal boxes, bottle carriers, can boxes. The present sequence is human protein. Note: There is no specific information about the sequence in the specification
XX	
SQ	Sequence 255 AA;
	Query Match 82.7%; Score 115; DB 7; Length 255;
	Best Local Similarity 80.0%; Pred. NO. 5e-09;
	Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY	1 CRPWTNCSLDGRSVLKTGTTEKDWW 25
DG	133 CRPWTNCSLDGKSVLVNGTKERDWW 157

RESULT 30
ADC78803
ID ADC78803 standard; protein; 255 AA.
XX
XX AC ADC78803;
XX
XX DT 01-JAN-2004 (first entry)
XX
XX DE Human PRO protein #16.
XX
XX KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
XX OS Homo sapiens.
XX
XX PN WO2003034984-A2.
XX
XX PD 01-MAY-2003.
XX
XX PF 15-OCT-2002; 2002WO-US033070.
XX
XX PR 19-OCT-2001; 2001US-0340083P.
XX
XX PA (GETH) GENENTECH INC.

Goddard A., Gurney AL;
WPI; 2003-481990/45.
N-PSDB; ADC78802.

New PRO polynucleotide and polypeptide, useful for the manufacture of a medicament for diagnosing or treating cancer or inflammatory bowel disorder e.g., ulcerative colitis or Crohn's disease.

Claim 12; SEQ ID NO 32; 327pp; English.

The invention comprises the amino acid and coding sequences of human PRO proteins. The DNA and protein sequences of the invention are useful for the diagnosis and treatment of cancer and inflammatory bowel disease (e.g. ulcerative colitis or Crohn's disease). The present amino acid sequence represents a human PRO protein of the invention.

Sequence 255 AA;

Query Match 82.7%; Score 115; DB 7; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0:

DQ 1 CRPWTNCSLDGRSVLKTGTTEKDW 25
 |||||::|||::|||:
Db 133 CRPWTNCSLDGRKSVLVNGTKERDW 157

RESULT 31
ADD25599
ID ADD25599 standard; protein; 255 AA.
AC ADD25599;
DT 15-JAN-2004 (first entry)
DE Binding domain-immunoglobulin fusion protein-associated protein #77.
KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
OS Unidentified.
PN US2003118592-A1.
PD 26-JUN-2003.
PF 25-JUL-2002; 2002US-00207655.
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-0005353O.
PR 03-JUN-2002; 2002US-0385691P.
PA (GENE-) GENECRAFT INC.
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
PP WPI; 2003-801317/75.
PT New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
PS Disclosure; SEQ ID NO 160; 157pp; English.
CC The invention relates to a binding domain-immunoglobulin fusion protein

comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 7; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 32
ADE87541

ID ADE87541 standard; protein; 255 AA.

AC ADE87541;

DT 29-JAN-2004 (first entry)

DE Unknown human receptor H4-1BB.

KW immunosuppressive; H4-1BB ligand binding blocker; human;
KW receptor protein; H4-1BB; B-cell proliferation stimulator;
KW T-cell proliferation enhancer; immune system suppressor; transplantation;
KW autoimmune disease.

OS Homo sapiens.

XX US2003082157-A1.

PD 01-MAY-2003.

PF 12-JUN-2002; 2002US-00170997.

XX 07-NOV-1988; 88US-00267577.
PR 30-JUL-1992; 92US-00922996.
PR 01-FEB-1993; 93US-00012269.
PR 05-JUN-1995; 95US-00460976.
PR 22-OCT-1997; 97US-00955573.
XX (KWON/) KWON B S.
XX Kwon BS;
XX WPI; 2003-576599/54.
DR N-PSDB; ADE87540.
XX New cDNA, or its encoded receptor protein H4-1BB, useful as probes to isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking H4-1BB ligand binding to facilitate organ transplantation or treat autoimmune diseases.
XX Disclosure; SEQ ID NO 2; 19pp; English.

XX The invention describes a cDNA, which encodes for human receptor protein H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe to isolate DNA sequences encoding for proteins similar to the receptor protein H4-1BB. The receptor protein H4-1BB, or its fragments or derivatives, is useful as a probe for identifying ligands to the receptor protein H4-1BB, or for stimulating the proliferation of B-cells expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are useful for enhancing T-cell proliferation of activation. The cDNA or receptor protein H4-1BB is also useful for blocking H4-1BB ligand binding, which is particularly useful for suppressing the immune system during transplantation, or for treating autoimmune diseases. This is the amino acid sequence of unknown human receptor H4-1BB.

XX SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 7; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 33

AAW04174
ID AAW04174 standard; protein; 255 AA.

AC AAW04174;

DT 12-DEC-1996 (first entry)

DE Human receptor H4-1BB.

KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW B-lymphocyte; B-cell; immunostimulant; cancer; autoimmune disease;
KW graft rejection; therapy.

OS Homo sapiens.

XX WO9629348-A1.

PD 26-SEP-1996.

PF 22-MAR-1996; 96WO-US003965.

PR 23-MAR-1995; 95US-00409851.

PA (INDV) UNIV INDIANA FOUND.

PI Kwon BS, Kang C;

XX

DR WPI; 1996-443138/44.
DR N-PSDB; AAT39546.
XX Monoclonal antibody specific for human receptor protein 4-1BB - used to
PT enhance proliferation and activation of T-cells for treatment of cancer
PT and to inhibit specific ligand binding for treating auto-immune diseases.
XX
XX Disclosure; Page 36-37; 48pp; English.
XX
XX Novel human receptor protein H4-1BB (AAW04174) has the potential to
CC function as an accessory signaling molecule during T-cell activation and
CC proliferation. Its amino acid sequence was deduced from a cDNA clone
CC (AAT39546) isolated from activated human T-lymphocytes. Recombinant H4-
CC 1BB can be produced in transfected host cells. It is used to isolate
CC receptor ligands, to stimulate B-cells expressing such ligands and to
CC block H4-1BB ligand binding. A fusion protein of H4-1BB with human
CC placental alkaline phosphatase can be used to modify immune responses. A
CC monoclonal antibody raised against an immunopeptide (see also AAW04172)
CC of H4-1BB is useful in the treatment of cancer and autoimmune diseases
XX
XX Sequence 255 AA;
SQ

Query Match 73.4%; Score 102; DB 2; Length 255;
Best Local Similarity 76.0%; Pred. No. 5.5e-07;
Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKEDVV 25
Db 133 CRPCTNCSLDGKSVLVNGTKERDVV 157

RESULT 34
AAY59508
ID AAY59508 standard; protein; 201 AA.
XX
AC AAY59508;
XX
DT 31-MAR-2000 (first entry)
XX
DE OBM binding protein sequence.
XX
KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;
KW bone metabolic disease; osteoporosis; therapy.
XX
OS Mus sp.
XX JP11332581-A.
XX
PD 07-DEC-1999.
XX
PF 20-OCT-1998; 98JP-00316973.
XX
PR 24-MAR-1998; 98JP-00076232.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2000-091362/08.
DR N-PSDB; AAZ49022.
XX
PT A new protein, a DNA and its application.
XX
PS Claim 1; Page 17-18; 18pp; Japanese.
XX
CC This sequence is the osteoclast formation promoting factor (OBM) binding
CC protein (OBM-BP) of the invention. The protein is useful as a preventive
CC and/or treating agent for bone metabolic diseases such as osteoporosis.
CC Substances which inhibit the binding of OBM to OBM-BP can be used as
CC biochemical reagents
XX
XX Sequence 201 AA;
SQ

Query Match 61.9%; Score 86; DB 3; Length 201;

Best Local Similarity 60.0%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKEDVV 25
Db 170 CKPWTNCTLLGKLEAHQQTESDVV 194

RESULT 35
ADB17000
ID ADB17000 standard; protein; 443 AA.
XX
AC ADB17000;
XX
DT 20-NOV-2003 (first entry)
XX
DE Murine RANK/ human Fc fusion protein with native RANK leader sequence.
XX
KW RANKL; RANK; receptor activator of nuclear factor-kappa B; ligand;
KW cytokine; immunoregulatory; TNF; tumour necrosis factor; TRAF;
KW TNF receptor associated factor; autoimmune; inflammatory; vaccine;
KW infectious disease; mouse; chimeric; IgG; immunoglobulin G; mutant;
KW mutein; murine.
XX
OS Chimeric.
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .213
FT /note= "RANK protein ({seqid:15}) residues 1-213 with
FT native leader sequence"
FT 214. .443
FT /note= "IGG mutein ({seqid:8}) residues 3-232"
XX
PN US2002086826-A1.
XX
PD 04-JUL-2002.
XX
PF 25-MAY-2001; 2001US-00865363.
XX
PR 23-DEC-1996; 96US-0059978P.
PR 07-MAR-1997; 97US-0077181P.
PR 14-OCT-1997; 97US-0064671P.
PR 22-DEC-1997; 97US-00995659.
PR 24-MAY-2000; 2000US-00577780.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM, Galibert L, Maraskovsky E;
XX
DR WPI; 2003-605660/57.
XX
PT Novel RANKL, ligand of receptor activator of nuclear factor-kappa B
PT useful for inducing maturation in dendritic cells and enhancing allo-
PT stimulatory capacity of dendritic cells.
XX
PS Example 15; Page; 49pp; English.
XX
CC This invention relates to a novel isolated RANKL polynucleotide and the
CC encoded protein thereof, where RANKL is the ligand of a novel receptor
CC referred to as RANK (Receptor Activator of Nuclear factor-Kappa B (NF-
CC kB)). Specifically, the invention describes this cytokine receptor/
CC ligand pair, and their role in immunoregulatory activity. RANK is a
CC member of the TNF (tumour necrosis factor) receptor superfamily and
CC shares similarity with TRAFs (TNF receptor associated factors), which are known
CC associates with TRAFs (TNF receptor associated factors), which are known
CC to play an important in the regulation of the immune and inflammatory
CC response. As such, RANK and RANKL can be used in the development of
CC diagnostics and therapeutics for use in autoimmune and inflammatory
CC diseases. Furthermore, the invention refers to preparing kits that are
CC used to detect soluble RANK or RANKL, for screening inhibitors of RANK,

CC for structure-based design of RANKL inhibitors, and in augmenting an
 CC immune response. It can also be useful as a vaccine adjuvant or a
 CC therapeutic agent to upregulate an immune response for example in
 CC infectious disease. This polypeptide sequence is a RANK/ Fc fusion
 CC protein comprising a soluble form of the murine RANK protein (with native
 CC leader sequence) fused to a mutant Fc region of human IgG, in an
 CC exemplification of the invention. NOTE: This sequence is not given in the
 CC specification but is derived from information provided in example 15.

XX SQ Sequence 443 AA;

Query Match 61.9%; Score 86; DB 7; Length 443;
 Best Local Similarity 60.0%; Pred. No. 0.00029;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 :|||||:|:|:|
 Db 170 CRPWTNCTLLGKLEAHQGTESDVV 194

RESULT 36
 AAW83200
 ID AAW83200 standard; protein; 625 AA.

XX AC AAW83200;

XX DT 11-FEB-1999 (first entry)

XX DE Murine osteoclast differentiation and activation receptor.

XX KW Osteoprotegerin binding protein; OPG binding protein; arthritis;
 XX KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
 XX KW hypercalcaemia; osteoclast differentiation and activation receptor;
 XX KW Paget's disease.

XX OS Mus sp.

XX PN WO9846751-A1.

XX PD 22-OCT-1998.

XX PF 15-APR-1998; 98WO-US007584.

XX PR 16-APR-1997; 97US-00842842.

XX PR 23-JUN-1997; 97US-00880855.

XX PR 30-MAR-1998; 98US-00052521.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ;

XX DR WPI; 1998-594578/50.

XX DR N-PSDB; AAV70304.

XX PT Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
 XX PT treating bone diseases by modulating osteoclast differentiation and for
 XX PT diagnosis.

XX PS Example 12; Fig 10; 47pp; English.

XX CC The present sequence represents murine osteoclast differentiation and
 CC activation receptor (ODAR). The present invention describes
 CC osteoprotegerin (OPG) binding protein. Host cells transfected with
 CC vectors containing nucleic acid molecules encoding OPG binding protein
 CC are used to produce recombinant OPG binding protein. OPG binding protein
 CC is used in binding assays to determine osteoprotegerin (OG) in biological
 CC samples; to screen for specific binding agents (particularly agonists and
 CC antagonists, including intracellular proteins); to raise Ab (useful in
 CC immunoassays for detection of OPG binding protein) and to identify
 CC compounds that modulate binding of OPG binding protein to ODAR. The
 CC nucleic acid molecule encoding OPG binding protein can be used to detect
 CC OPG binding protein-encoding sequences, e.g. screening for related
 CC sequences, also to produce transgenic animal models, while complementary

CC sequences are used for antisense regulation of OPG binding protein
 CC expression. Modulators of OPG binding protein, particularly soluble forms
 CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,
 CC e.g. osteoporosis, bone loss caused by arthritis or metastases,
 CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,
 CC loosening of prostheses, optionally in combination with agents that
 CC promote bone growth

XX SQ Sequence 625 AA;

Query Match 61.9%; Score 86; DB 2; Length 625;
 Best Local Similarity 60.0%; Pred. No. 0.00043;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 :|||||:|:|:|
 Db 170 CRPWTNCTLLGKLEAHQGTESDVV 194

RESULT 37
 AAW69958
 ID AAW69958 standard; protein; 625 AA.

XX AC AAW69958;

XX DT 08-OCT-1998 (first entry)

XX DE Murine NF-kB receptor activator muRANK.

XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 XX KW immune response; inflammatory response; toxic shock; sepsis; RANKL;
 XX KW RANK ligand; tumour necrosis factor; TNF; murine.

XX OS Mus sp.

XX PN WO9828426-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US023775.

XX PR 23-DEC-1996; 96US-0059978P.

XX PR 07-MAR-1997; 97US-00813509.

XX PR 14-OCT-1997; 97US-0064671P.

XX PA (IMMV) IMMUNEX CORP.

XX PI Anderson DM, Galibert LJ, Maraskovsky E;

XX DR WPI; 1998-377657/32.

XX DR N-PSDB; AAV41379.

XX PT New isolated ligand for receptor activator of NF-kappa B - used to
 XX PT develop products for augmenting an immune response for inhibiting an
 XX PT inflammatory response and for protection of cells.

XX PS Example 14; Page 62-64; 80pp; English.

XX CC This represents the murine muRANK (receptor activator of necrosis factor-
 CC kappaB (NF-kB)) polypeptide which is a homolog of the human RANK. RANK is
 CC a member of the tumour necrosis factor (TNF) family. A soluble RANK may
 CC be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used
 CC to induce maturation of dendritic cells and enhance their allo-
 CC stimulatory capacity, thereby augmenting an immune response. The soluble
 CC RANK polypeptide composition may also be used for regulating an immune or
 CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be
 CC useful in ameliorating negative effects of an inflammatory response that
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
 CC graft-versus-host reactions, or acute inflammatory reactions. They can
 CC also be used in adjunct therapy for disease characterised by neoplastic
 CC cells that express RANK. RANKL polypeptides can also be used to identify

CC inhibitors of RANK and thus inhibitors of an inflammatory response, and
CC also for protecting RANK-expressing cells from the negative effects of
CC chemotherapy or the presence of high levels of TNF-alpha. The products
CC can also be used for detection and drug screening

XX Sequence 625 AA;
SQ
Query Match 61.9%; Score 86; DB 2; Length 625;
Best Local Similarity 60.0%; Pred. No. 0.00043;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

RESULT 38
AAW68294
ID AAW68294 standard; protein; 625 AA.
XX
AC AAW68294;
XX
XX 08-OCT-1998 (first entry)
XX Murine NF-kB receptor activator muRANK.
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis; RANKL;
KW RANK ligand; tumour necrosis factor; TNF; murine.
XX
OS Mus sp.
XX WO9828424-A2.
PN
XX
PD 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US023866.
XX
XX 23-DEC-1996; 96US-0059978P.
PR 07-MAR-1997; 97US-00813509.
PR 14-OCT-1997; 97US-0064671P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
PI
XX WPI; 1998-377655/32.
DR N-PSDB; AAV41373.
XX
XX New isolated receptor activator of necrosis factor-kappa B - useful for,
PT e.g. developing products for regulating an immune or inflammatory
PT response, treating toxic shock or sepsis.
XX
XX Claim 27; Page 62-64; 80pp; English.

XX This represents the murine muRANK (receptor activator of necrosis factor-
CC kappaB (NF-kB)) polypeptide which is a homolog of the human RANK. RANK is
CC a member of the tumour necrosis factor (TNF) family. Host cells
CC transformed or transfected with an expression vector comprising the RANK
CC encoding nucleic acid can be used to produce recombinant RANK protein.
CC The soluble RANK may be used for inhibiting activation of NF-kB, by
CC contacting a cell expressing membrane-associated RANK with a soluble RANK
CC which binds to RANK ligand (RANKL). The soluble RANK polypeptide
CC composition may also be used for regulating an immune or inflammatory
CC response. Inhibition of NF-kB by RANK antagonists may be useful in
CC ameliorating negative effects of an inflammatory response that result
CC from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-
CC versus-host reactions, or acute inflammatory reactions. They can also be
CC used in adjunct therapy for disease characterised by neoplastic cells
CC that express RANK. The products can also be used for detection and drug
CC screening
XX
XX Sequence 625 AA;

Query Match 61.9%; Score 86; DB 2; Length 625;
Best Local Similarity 60.0%; Pred. No. 0.00043;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

RESULT 39
AAE08739
ID AAE08739 standard; protein; 625 AA.
XX
XX AAE08739;
XX
XX 15-NOV-2001 (first entry)
XX Murine receptor activator of NF kappaB (RANK) protein.
XX
XX Murine; receptor activator of nuclear factor kappaB; RANK; NF;
KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
KW immune response; inflammatory response; graft-versus-host reaction;
KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX Mus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1. .30
FT /label= Signal_peptide
FT Protein 31. .625
FT /label= Mature_RANK_protein
XX
XX US6271349-B1.
XX
XX 07-AUG-2001.
XX
XX 17-DEC-1998; 98US-00215649.
XX
XX 23-DEC-1996; 96US-0059978P.
PR 23-DEC-1996; 96US-00772330.
PR 07-MAR-1997; 97US-0077181P.
PR 07-MAR-1997; 97US-00813509.
PR 14-OCT-1997; 97US-0064671P.
PR 22-DEC-1997; 97US-00996139.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Dougall WC, Galibert L;
PI
XX WPI; 1998-377655/32.
DR N-PSDB; AAD15312.
XX
XX New isolated receptor activator of necrosis factor-kappa B - useful for,
PT e.g. developing products for regulating an immune or inflammatory
PT response, treating toxic shock or sepsis.
XX
XX Example 14; Col 77-80; 47pp; English.

XX The patent discloses novel receptor activator of nuclear factor (NF)-
CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of
CC the tumour necrosis factor (TNF) receptor superfamily and associates with
CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the
CC regulation of immune and inflammatory response. The receptors are useful
CC for regulating immune response and in screening for inhibitors of these
CC receptors. The cytoplasmic domain of RANK is used in developing assays
CC for inhibitors of signal transduction, e.g. for screening the molecules
CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and
CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful
CC in ameliorating the negative effects of an inflammatory response that
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
CC graft-versus-host reactions, acute inflammatory reactions and the effects

CC of bone resorption. RANK acts as an anti- apoptotic signal and rescue the
 CC cells that express RANK from apoptosis. Soluble forms of the receptor are
 CC used in vivo or in vitro based screening tests for agonists or
 CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B
 CC activation, or to inhibit transduction of a signal via RANK. RANK
 CC compositions are used in the development of both agonistic and
 CC antagonistic antibodies, or as an adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. Compounds that
 CC interfere with RANK/TRAFF6 interactions are useful for modulating the
 CC formation of osteoclasts from osteoclast precursors and for modulating
 CC osteoclast function and activities. They are used as inhibitors of
 CC diseases associated with excess bone resorption and as immunosuppressants
 CC or anti-inflammatory agents. The RANK DNAs are useful for the expression
 CC of recombinant proteins, as probes for analysis of the presence or
 CC distribution of RANK transcripts, while the proteins are useful in
 CC preparing kits for the detection of soluble RANK, or monitor RANK-related
 CC activity. The present sequence is RANK protein from murine
 XX
 SQ Sequence 625 AA;

Query Match 61.9%; Score 86; DB 2; Length 625;
 Best Local Similarity 60.0%; Pred. No. 0.00043;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

RESULT 40
 AAY53649
 ID AAY53649 standard; protein; 625 AA.

AC AAY53649;

DT 22-FEB-2000 (first entry)

DE A mouse receptor activator of NF-kappaB designated RANK.

KW Mouse; receptor; RANK; Receptor activator of NF-kappaB;
 KW osteoclast activity; immune response; inflammatory response;
 KW excess bone resorption; osteoclast generation; bone loss; osteoporosis;
 KW Paget's disease; bone cancer; cancer; hypercalcaemia; osteoclastogenesis;
 KW metastasising cancer; osteoclast differentiation; signal transduction.

OS Mus sp.

XX WO9958674-A2.

XX 18-NOV-1999.

XX 13-MAY-1999; 99WO-US010588.

XX 14-MAY-1998; 98US-0085487P.

PR 03-DEC-1998; 98US-0110836P.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ;

XX WPI; 2000-053099/04.

DR N-PSDB; AA236258.

PT Novel cytokine receptors for regulating osteoclast activity to ameliorate
 PT excess bone loss effects of osteoporosis, Paget's disease, bone cancers
 PT etc.

PS Disclosure; Page 25-27; 28pp; English.

CC The present sequence represents a soluble murine receptor designated RANK
 CC (Receptor activator of NF-kappaB). The protein is used to regulate
 CC osteoclast activity. The RANK protein or its fragments are useful for
 CC regulating an immune or inflammatory response, especially to decrease

CC excess bone resorption, and for inhibiting osteoclast activity,
 CC regulating osteoclast generation and inhibiting osteoclast generation in
 CC individuals inflicted with excess bone resorption. Especially, the RANK
 CC protein is used to treat individuals at risk for excess bone loss,
 CC osteoporosis, Paget's disease, bone cancer and cancers associated with
 CC hypercalcaemia. The RANK protein ameliorates the effects of excess bone
 CC loss, by binding to its ligand and inhibiting binding of other cells
 CC expressing RANK. It thus decreases osteoclastogenesis when administered
 CC into metastasising cancers such as breast cancer, multiple myeloma,
 CC melanomas, lung cancer, prostate, hematologic, head and neck, and renal
 CC which metastasise to bone and induce bone breakdown by locally disrupting
 CC normal bone remodelling, by disrupting the osteoclast differentiation
 CC pathway. This results in the reduction in the number of osteoclasts,
 CC lesser bone resorption and relief from the negative effects of
 CC hypercalcaemia. The RANK protein also ameliorates systemic effects by
 CC interfering with I/II signal transduction that leads to the
 CC differentiation of osteoclast precursors into osteoclasts
 XX
 SQ Sequence 625 AA;

Query Match 61.9%; Score 86; DB 3; Length 625;
 Best Local Similarity 60.0%; Pred. No. 0.00043;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

Search completed: May 5, 2004, 14:38:05
 Job time : 13.4144 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:35:32 ; Search time 3.59589 Seconds
(without alignments)
358.923 Million cell updates/sec

Title: US-10-067-122B-2_COPY_133_157
Perfect score: 139
Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVW 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	191	3	US-08-974-022-52
2	139	100.0	191	3	US-08-795-445A-52
3	139	100.0	191	3	US-08-795-447A-52
4	139	100.0	191	3	US-08-974-186-52
5	139	100.0	191	3	US-08-795-446B-52
6	139	100.0	191	4	US-08-706-945D-139
7	139	100.0	191	4	US-08-577-788C-53
8	139	100.0	256	1	US-08-236-918A-6
9	139	100.0	256	4	US-09-150-864A-6
10	139	100.0	256	4	US-08-012-269A-2
11	139	100.0	256	4	US-09-623-545A-3
12	139	100.0	256	5	PCT-US96-03965-2
13	115	82.7	132	4	US-09-523-323-55
14	115	82.7	219	2	US-08-816-605-2
15	115	82.7	255	1	US-08-236-918A-8
16	115	82.7	255	2	US-08-816-605-9
17	115	82.7	255	3	US-09-006-353A-11
18	115	82.7	255	4	US-09-007-097-2
19	115	82.7	255	4	US-09-150-864A-8
20	115	82.7	255	4	US-09-573-986-11
21	115	82.7	255	4	US-09-578-764A-2
22	115	82.7	255	4	US-09-623-545A-2
23	115	82.7	255	5	PCT-US96-03965-8
24	86	61.9	625	3	US-08-996-139-15
25	86	61.9	625	3	US-08-995-659-15
26	86	61.9	625	3	US-09-215-649A-15
27	86	61.9	625	4	US-09-577-780-15

28	86	61.9	625	4	US-09-577-800-15	Sequence 15, Appl
29	86	61.9	625	4	US-09-466-496-15	Sequence 15, Appl
30	86	61.9	625	4	US-09-871-856-15	Sequence 15, Appl
31	86	61.9	625	4	US-09-871-291-15	Sequence 15, Appl
32	86	61.9	625	4	US-09-877-650-15	Sequence 15, Appl
33	75	54.0	451	3	US-08-996-139-4	Sequence 4, Appli
34	75	54.0	451	3	US-08-995-659-4	Sequence 4, Appli
35	75	54.0	451	3	US-09-215-649A-4	Sequence 4, Appli
36	75	54.0	451	4	US-09-577-780-4	Sequence 4, Appli
37	75	54.0	451	4	US-09-577-800-4	Sequence 4, Appli
38	75	54.0	451	4	US-09-466-496-4	Sequence 4, Appli
39	75	54.0	451	4	US-09-871-856-4	Sequence 4, Appli
40	75	54.0	451	4	US-09-871-291-4	Sequence 4, Appli
41	75	54.0	451	4	US-09-877-650-4	Sequence 4, Appli
42	75	54.0	591	3	US-08-996-139-2	Sequence 2, Appli
43	75	54.0	591	3	US-08-995-659-2	Sequence 2, Appli
44	75	54.0	591	3	US-09-215-649A-2	Sequence 2, Appli
45	75	54.0	591	4	US-09-577-780-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-974-022-52
; Sequence 52, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, Willaim J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-52

Query Match 100.0%; Score 139; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVW 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVW 157

RESULT 2
US-08-795-445A-52
; Sequence 52, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-445A-52

Query Match 100.0%; Score 139; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 3
US-08-795-447A-52
; Sequence 52, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-447A-52

Query Match 100.0%; Score 139; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 4
US-08-974-186-52
; Sequence 52, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-52

Query Match 100.0%; Score 139; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 5

US-08-795-446B-52
; Sequence 52, Application US/08795446B
; Patent No. 6289032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-446B-52

Query Match 100.0%; Score 139; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 6

US-08-706-945D-139
; Sequence 139, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 139
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-139

Query Match 100.0%; Score 139; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 7

US-08-577-788C-53
; Sequence 53, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-577-788C-53

Query Match 100.0%; Score 139; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 8

US-08-236-918A-6
; Sequence 6, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843

```
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-6

Query Match      100.0%; Score 139; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db      133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 9
US-09-150-864A-6
; Sequence 6, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus sp. (clone: mu4-1BB)
; US-09-150-864A-6

Query Match      100.0%; Score 139; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db      133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 10
US-08-012-269A-2
; Sequence 2, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13

; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-6

Query Match      100.0%; Score 139; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db      133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 11
US-09-623-545A-3
; Sequence 3, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; TITLE OF INVENTION: PROLIFERATION OF PERIPHERAL MONOCYTES
; FILE REFERENCE: 30424.1USWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-623-545A-3

Query Match      100.0%; Score 139; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db      133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 12
PCT-US96-03965-2
; Sequence 2, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-Yuil
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03965
; FILING DATE:
; CLASSIFICATION:
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KW05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-03965-2

```

```

Query Match 100.0%; Score 139; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

```

RESULT 13

```

US-09-523-323-55
; Sequence 55, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/168,380
; EARLIER FILING DATE: 1999-12-02
; EARLIER APPLICATION NUMBER: 60/148,326
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/142,657
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 60/137,457
; EARLIER FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: 60/124,041
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 09/252,656
; EARLIER FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: 60/075,409
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/027,287
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: 60/013,923
; EARLIER FILING DATE: 1996-03-22
; EARLIER APPLICATION NUMBER: 60/030,157

```

```

; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-523-323-55

```

```

Query Match 82.7%; Score 115; DB 4; Length 132;
Best Local Similarity 80.0%; Pred. No. 2e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 106 CRPWTNCSLDGKSVLVNGTKERDVV 130

```

RESULT 14

```

US-08-816-605-2
; Sequence 2, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-605-2

```

```

Query Match 82.7%; Score 115; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 3.7e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 97 CRPWTNCSLDGKSVLVNGTKERDVV 121

```

RESULT 15

```

US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:

```

```

; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-8

```

Query Match 82.7%; Score 115; DB 1; Length 255;
 Best Local Similarity 80.0%; Pred. No. 4.4e-10;
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

```

```

RESULT 16
US-08-816-605-9
; Sequence 9, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,605

```

```

; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-816-605-9

```

Query Match 82.7%; Score 115; DB 2; Length 255;
 Best Local Similarity 80.0%; Pred. No. 4.4e-10;
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

```

```

RESULT 17
US-09-006-353A-11
; Sequence 11, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-006-353A-11

```

Query Match 82.7%; Score 115; DB 3; Length 255;
 Best Local Similarity 80.0%; Pred. No. 4.4e-10;
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |||||:|||||:|||||:|||||:|||||
Db     133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 18
US-09-007-097-2
; Sequence 2, Application US/09007097A
; Patent No. 6303121
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/007,097A
; CURRENT FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-007-097-2

Query Match      82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |||||:|||||:|||||:|||||:|||||
Db     133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 19
US-09-150-864A-8
; Sequence 8, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens (clone: hu4-1BB)
US-09-150-864A-8

Query Match      82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |||||:|||||:|||||:|||||:|||||
Db     133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 20
US-09-573-986-11
; Sequence 11, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
```

```
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-11

Query Match      82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |||||:|||||:|||||:|||||:|||||
Db     133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 21
US-09-578-764A-2
; Sequence 2, Application US/09578764A
; Patent No. 6569997
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/578,764A
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-578-764A-2

Query Match      82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |||||:|||||:|||||:|||||:|||||
Db     133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 22
US-09-623-545A-2
; Sequence 2, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; FILE REFERENCE: 30424.1USWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-545A-2

Query Match      82.7%; Score 115; DB 4; Length 255;
```


MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-15

Query Match 61.9%; Score 86; DB 3; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|
Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

RESULT 26

US-09-215-649A-15
; Sequence 15, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

Query Match 61.9%; Score 86; DB 3; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|
Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

RESULT 27

US-09-577-780-15
; Sequence 15, Application US/09577780
; Patent No. 6419929
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid

```
/
/      TOPOLOGY: linear
/      MOLECULE TYPE: protein
/      SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15
Query Match      61.9%; Score 86; DB 4; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |:|||||:|:|:|||||
Db      170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 28
US-09-577-800-15
; Sequence 15, Application US/09577800
; Patent No. 6479635
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,800
; FILING DATE: 24-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/996,139
; FILING DATE: 22 DECEMBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-577-800-15
Query Match      61.9%; Score 86; DB 4; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |:|||||:|:|:|||||
Db      170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 29
US-09-466-496-15
; Sequence 15, Application US/09466496
; Patent No. 6528482
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,496
; FILING DATE: 17-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-466-496-15
Query Match      61.9%; Score 86; DB 4; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |:|||||:|:|:|||||
Db      170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 30
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
```

```
Db      170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 29
US-09-466-496-15
; Sequence 15, Application US/09466496
; Patent No. 6528482
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,496
; FILING DATE: 17-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-466-496-15
Query Match      61.9%; Score 86; DB 4; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |:|||||:|:|:|||||
Db      170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 30
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
```

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation, Law Department
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Power Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.5.5
/ SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/871,856
/ FILING DATE: 31-May-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/996,139
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: USSN 08/813,509
/ FILING DATE: 07 MARCH 1997
/ APPLICATION NUMBER: USSN 08/772,330
/ FILING DATE: 23 DECEMBER 1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2851-A
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 625 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

Query Match 61.9%; Score 86; DB 4; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|||||
Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 31
US-09-871-291-15
; Sequence 15, Application US/09871291
; Patent No. 6562948
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,291
; FILING DATE: 30-May-2001
```

```
/
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/996,139
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: USSN 08/813,509
/ FILING DATE: 07 MARCH 1997
/ APPLICATION NUMBER: USSN 08/772,330
/ FILING DATE: 23 DECEMBER 1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2851-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 625 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-291-15

Query Match 61.9%; Score 86; DB 4; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|||||
Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 32
US-09-877-650-15
; Sequence 15, Application US/09877650
; Patent No. 6649164
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
```

;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 625 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-877-650-15

Query Match 61.9%; Score 86; DB 4; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|
Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 33
US-08-996-139-4
; Sequence 4, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-4

Query Match 54.0%; Score 75; DB 3; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 35
US-09-215-649A-4
; Sequence 4, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent

Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193
|:|||||:|:|

RESULT 34
US-08-995-659-4
; Sequence 4, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-4

Query Match 54.0%; Score 75; DB 3; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 35
US-09-215-649A-4
; Sequence 4, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent

;; Maraskovsky, Eugene
;; TITLE OF INVENTION: Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/215,649A
;; FILING DATE: 17-Dec-1998
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/996,139
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;;
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 451 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-215-649A-4

Query Match 54.0%; Score 75; DB 3; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|||||:|:|:|:|
Db 169 CRPWTNCTFLGKRVEHGTGTEKSDAV 193

RESULT 36
US-09-577-780-4
; Sequence 4, Application US/09577780
; Patent No. 6419929
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/577,780
;; FILING DATE: 24-May-2000
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/995,659
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2852-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;;
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 451 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-577-780-4

Query Match 54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|||||:|:|:|:|
Db 169 CRPWTNCTFLGKRVEHGTGTEKSDAV 193

RESULT 37
US-09-577-800-4
; Sequence 4, Application US/09577800
; Patent No. 6479635
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,800
; FILING DATE: 24-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/996,139
; FILING DATE: 22 DECEMBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330

```
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-577-800-4

Query Match 54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 38
US-09-466-496-4
; Sequence 4, Application US/09466496
; Patent No. 6528482
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,496
; FILING DATE: 17-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-466-496-4

Query Match 54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 39
US-09-871-856-4
; Sequence 4, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-871-856-4

Query Match 54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 40
US-09-871-291-4
; Sequence 4, Application US/09871291
```


Patent No. 6562948
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,291
FILING DATE: 30-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-871-291-4

Query Match 54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTETKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

Search completed: May 5, 2004, 14:42:17
Job time : 4.59589 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:40:42 ; Search time 9.24658 Seconds
(without alignments)
749.438 Million cell updates/sec

Title: US-10-067-122B-2_COPY_133_157
Perfect score: 139
Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	139	100.0	191	11 US-09-405-032-136	Sequence 136, Appl
2	139	100.0	256	13 US-10-027-199-10	Sequence 10, Appl
3	139	100.0	256	14 US-10-067-122-2	Sequence 2, Appli
4	115	82.7	132	15 US-10-375-680-55	Sequence 55, Appl
5	115	82.7	219	9 US-09-739-394-2	Sequence 2, Appli
6	115	82.7	219	13 US-10-097-330-2	Sequence 2, Appli
7	115	82.7	255	9 US-09-739-394-9	Sequence 9, Appli
8	115	82.7	255	9 US-09-826-212-11	Sequence 11, Appl
9	115	82.7	255	9 US-09-935-727-13	Sequence 13, Appl
10	115	82.7	255	10 US-09-877-336-2	Sequence 2, Appli
11	115	82.7	255	13 US-10-097-330-9	Sequence 9, Appli
12	115	82.7	255	13 US-10-027-199-2	Sequence 2, Appli
13	115	82.7	255	14 US-10-170-997-2	Sequence 2, Appli
14	115	82.7	255	14 US-10-186-643-11	Sequence 11, Appl
15	115	82.7	255	14 US-10-207-655-160	Sequence 160, App

16	115	82.7	255	15	US-10-418-242-13	Sequence 13, Appl
17	86	61.9	625	9	US-09-871-856-15	Sequence 15, Appl
18	86	61.9	625	9	US-09-877-650-15	Sequence 15, Appl
19	86	61.9	625	12	US-09-865-363-15	Sequence 15, Appl
20	86	61.9	625	12	US-10-151-071-2	Sequence 2, Appli
21	86	61.9	625	12	US-09-957-944-4	Sequence 4, Appli
22	86	61.9	625	14	US-10-166-232A-2	Sequence 2, Appli
23	86	61.9	625	14	US-10-405-878-15	Sequence 15, Appl
24	79	56.8	615	9	US-09-768-779A-2	Sequence 2, Appli
25	79	56.8	615	14	US-10-291-480-2	Sequence 2, Appli
26	75	54.0	443	12	US-10-151-071-5	Sequence 5, Appli
27	75	54.0	443	14	US-10-166-232A-5	Sequence 4, Appli
28	75	54.0	451	9	US-09-871-856-4	Sequence 4, Appli
29	75	54.0	451	9	US-09-877-650-4	Sequence 4, Appli
30	75	54.0	451	12	US-09-865-363-4	Sequence 4, Appli
31	75	54.0	451	14	US-10-405-878-4	Sequence 4, Appli
32	75	54.0	591	9	US-09-871-856-2	Sequence 2, Appli
33	75	54.0	591	9	US-09-877-650-2	Sequence 2, Appli
34	75	54.0	591	12	US-09-865-363-2	Sequence 2, Appli
35	75	54.0	591	14	US-10-405-878-2	Sequence 2, Appli
36	75	54.0	616	9	US-09-871-856-6	Sequence 6, Appli
37	75	54.0	616	9	US-09-877-650-6	Sequence 6, Appli
38	75	54.0	616	12	US-09-865-363-6	Sequence 6, Appli
39	75	54.0	616	12	US-10-151-071-4	Sequence 4, Appli
40	75	54.0	616	12	US-09-957-944-2	Sequence 2, Appli
41	75	54.0	616	14	US-10-166-232A-4	Sequence 4, Appli
42	75	54.0	616	14	US-10-405-878-6	Sequence 6, Appli
43	75	54.0	622	12	US-09-957-944-10	Sequence 10, Appl
44	73	52.5	138	13	US-10-112-793-20	Sequence 20, Appl
45	73	52.5	274	9	US-09-836-607-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-405-032-136
; Sequence 136, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-405-032-136

Query Match 100.0%; Score 139; DB 11; Length 191;

Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 2

US-10-027-199-10
; Sequence 10, Application US/10027199
; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-027-199-10

Query Match 100.0%; Score 139; DB 13; Length 256;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 3

US-10-067-122-2
; Sequence 2, Application US/10067122
; Publication No. US20030100745A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/10/067,122
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 08/012,269
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-122-2

Query Match 100.0%; Score 139; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 4
US-10-375-680-55
; Sequence 55, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000E
; CURRENT APPLICATION NUMBER: US/10/375,680
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,234
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-375-680-55

Query Match 82.7%; Score 115; DB 15; Length 132;
Best Local Similarity 80.0%; Pred. No. 2e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 106 CRPWTNCSLDGRSVLKTGTTEKDVV 130

RESULT 5

US-09-739-394-2
; Sequence 2, Application US/09739394
; Patent No. US20010014465A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,394
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/253,549
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

LENGTH: 219 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2;
US-09-739-394-2

Query Match 82.7%; Score 115; DB 9; Length 219;
Best Local Similarity 80.0%; Pred. No. 3.4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 97 CRPWTNCSLDGKSVLVNGTKERDVV 121

RESULT 6
US-10-097-330-2
Sequence 2, Application US/10097330
Publication No. US20020127651A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
FILE REFERENCE: PF254D1C2
CURRENT APPLICATION NUMBER: US/10/097,330
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/739,394
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/253,549
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: US 08/816,605
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 60/013,474
PRIOR FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-330-2

Query Match 82.7%; Score 115; DB 13; Length 219;
Best Local Similarity 80.0%; Pred. No. 3.4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 97 CRPWTNCSLDGKSVLVNGTKERDVV 121

RESULT 7
US-09-739-394-9
Sequence 9, Application US/09739394
Patent No. US20010014465A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Yu, Guo-Liang
Gentz, Reiner
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,394
FILING DATE: 19-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/253,549
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9;
US-09-739-394-9

Query Match 82.7%; Score 115; DB 9; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 8
US-09-826-212-11
Sequence 11, Application US/09826212
Patent No. US20010021516A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
Gentz, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280006
CURRENT APPLICATION NUMBER: US/09/826,212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-212-11

Query Match 82.7%; Score 115; DB 9; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 9
US-09-935-727-13
Sequence 13, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24

```

; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-13

```

```

Query Match      82.7%; Score 115; DB 9; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDV 25
Db      133 CRPWTNCSLDGKSVLVNGTKERDV 157

```

```

RESULT 10
US-09-877-336-2
; Sequence 2, Application US/09877336
; Publication No. US2003000851A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHODS OF USING HUMAN RECEPTOR ON
; FILE OF INVENTION: PROTEIN 4-1BB
; FILE REFERENCE: 740.011US3
; CURRENT APPLICATION NUMBER: US/09/877,336
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 09/007,097
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: 08/409,851
; PRIOR FILING DATE: 1995-03-23
; PRIOR APPLICATION NUMBER: 08/122,796
; PRIOR FILING DATE: 1993-09-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-877-336-2

```

```

Query Match      82.7%; Score 115; DB 10; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDV 25
Db      133 CRPWTNCSLDGKSVLVNGTKERDV 157

```

```

RESULT 11
US-10-097-330-9
; Sequence 9, Application US/10097330
; Publication No. US20020127651A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
; FILE REFERENCE: PF254D1C2
; CURRENT APPLICATION NUMBER: US/10/097,330
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/739,394
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/253,549
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: US 08/816,605
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 60/013,474
; PRIOR FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-330-9

```

```

Query Match      82.7%; Score 115; DB 13; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDV 25
Db      133 CRPWTNCSLDGKSVLVNGTKERDV 157

```

```

RESULT 12
US-10-027-199-2
; Sequence 2, Application US/10027199
; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-199-2

```

```

Query Match      82.7%; Score 115; DB 13; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDV 25
Db      133 CRPWTNCSLDGKSVLVNGTKERDV 157

```

```

RESULT 13
US-10-170-997-2

```



```

; Sequence 2, Application US/10170997
; Publication No. US20030082157A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: New Receptor and Related Products and
;   METHODS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/170,997
; FILING DATE: 12-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,573
; FILING DATE: 22-OCT-1997
; APPLICATION NUMBER: 08/460,976
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 13-SEP-1993
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; APPLICATION NUMBER: US 08/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KWO4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-170-997-2

```

```

Query Match      82.7%; Score 115; DB 14; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db      133 CRPWTNCSLDGRSVLVNGTKERDV 157

RESULT 14
US-10-186-643-11
; Sequence 11, Application US/10186643
; Publication No. US20030118546A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/10/186,643

```

```

; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-643-11

Query Match      82.7%; Score 115; DB 14; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db      133 CRPWTNCSLDGRSVLVNGTKERDV 157

RESULT 15
US-10-207-655-160
; Sequence 160, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-160

```

```

Query Match      82.7%; Score 115; DB 14; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db      133 CRPWTNCSLDGRSVLVNGTKERDV 157

```

```

RESULT 16
US-10-418-242-13
; Sequence 13, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P3
; CURRENT APPLICATION NUMBER: US/10/418,242
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,604
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371

```

;; PRIOR FILING DATE: 1999-08-02
;; PRIOR APPLICATION NUMBER: 60/131,964
;; PRIOR FILING DATE: 1999-04-30
;; PRIOR APPLICATION NUMBER: 60/131,279
;; PRIOR FILING DATE: 1999-04-27
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 51
;; SEQ ID NO 13
;; LENGTH: 255
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-418-242-13

Query Match 82.7%; Score 115; DB 15; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 17
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

Query Match 61.9%; Score 86; DB 9; Length 625;
Best Local Similarity 60.0%; Pred. No. 0.00026;

Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194
RESULT 18
US-09-877-650-15
; Sequence 15, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-877-650-15

Query Match 61.9%; Score 86; DB 9; Length 625;
Best Local Similarity 60.0%; Pred. No. 0.00026;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

RESULT 19
US-09-865-363-15
; Sequence 15, Application US/09865363
; Publication No. US20020086826A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation, Law Department
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/865,363
 ; FILING DATE: 25-May-2001
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/995,659
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: USSN 08/813,509
 ; FILING DATE: 07 MARCH 1997
 ; APPLICATION NUMBER: USSN 08/772,330
 ; FILING DATE: 23 DECEMBER 1996
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2852-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)233-0644
 ;
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 625 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 ;
 ; US-09-865-363-15

Query Match 61.9%; Score 86; DB 12; Length 625;
 Best Local Similarity 60.0%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 |:|||||:|:|:|||||
 Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194
 |:|||||:|:|:|||||
 RESULT 20
 US-10-151-071-2
 ; Sequence 2, Application US/10151071
 ; Publication No. US20030017151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DOUGALL, William
 ; APPLICANT: ANDERSON, Dirk
 ; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
 ; FILE REFERENCE: 3277-A
 ; CURRENT APPLICATION NUMBER: US/10/151,071
 ; CURRENT FILING DATE: 2001-05-17
 ; PRIOR APPLICATION NUMBER: 60/291,919
 ; PRIOR FILING DATE: 2001-05-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 625
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ;
 ; US-10-151-071-2

Query Match 61.9%; Score 86; DB 12; Length 625;
 Best Local Similarity 60.0%; Pred. No. 0.00026;

Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 |:|||||:|:|:|||||
 Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194
 |:|||||:|:|:|||||
 RESULT 21
 US-09-957-944-4
 ; Sequence 4, Application US/09957944
 ; Publication No. US20020086312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dougall, William C.
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVAT
 ; TITLE OF INVENTION: NF-kappa B
 ; FILE REFERENCE: 3109-A
 ; CURRENT APPLICATION NUMBER: US/09/957,944
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: 60/235,157
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 625
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ;
 ; US-09-957-944-4

Query Match 61.9%; Score 86; DB 12; Length 625;
 Best Local Similarity 60.0%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 |:|||||:|:|:|||||
 Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194
 |:|||||:|:|:|||||
 RESULT 22
 US-10-166-232A-2
 ; Sequence 2, Application US/10166232A
 ; Publication No. US20030021785A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DOUGALL, William, C.
 ; TITLE OF INVENTION: USE OF RANK ANTAGONISTS TO TREAT CANCER
 ; FILE REFERENCE: 3278-A
 ; CURRENT APPLICATION NUMBER: US/10/166,232A
 ; CURRENT FILING DATE: 2002-06-05
 ; PRIOR APPLICATION NUMBER: 60/296,670
 ; PRIOR FILING DATE: 2001-06-06
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 625
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ;
 ; US-10-166-232A-2

Query Match 61.9%; Score 86; DB 14; Length 625;
 Best Local Similarity 60.0%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 |:|||||:|:|:|||||
 Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194
 |:|||||:|:~|:|||||
 RESULT 23
 US-10-405-878-15
 ; Sequence 15, Application US/10405878
 ; Publication No. US20030175840A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Dirk M.
 ; Galibert, Laurent

```

; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/405,878
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-405-878-15

Query Match 61.9%; Score 86; DB 14; Length 625;
Best Local Similarity 60.0%; Pred. No. 0.00026;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|:|
Db 170 CKPWTNCTLLGKLEAHQGTESDVV 194

RESULT 24
US-09-768-779A-2
; Sequence 2, Application US/09768779A
; Patent No. US20020127637A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/768,779A
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/086,582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KENLEY K. HOOVER
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF368PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-768-779A-2

Query Match 56.8%; Score 79; DB 9; Length 615;
Best Local Similarity 56.0%; Pred. No. 0.0029;
Matches 14; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|:|
Db 168 CRPWTNCTFLGKRVEHHGTEKSDVV 192

RESULT 25
US-10-291-480-2
; Sequence 2, Application US/10291480
; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PF368C1D1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/768,779
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/086,582
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/048,020
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 615
; TYPE: PRT
; ORGANISM: human
US-10-291-480-2

Query Match 56.8%; Score 79; DB 14; Length 615;
Best Local Similarity 56.0%; Pred. No. 0.0029;
Matches 14; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:|:|
Db 168 CRPWTNCTFLGKRVEHHGTEKSDVV 192

RESULT 26
US-10-151-071-5
; Sequence 5, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:

```

APPLICANT: DOUGALL, William
APPLICANT: ANDERSON, Dirk
TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
FILE REFERENCE: 3277-A
CURRENT APPLICATION NUMBER: US/10/151,071
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/291,919
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 443
TYPE: PRT
ORGANISM: Homo sapiens
US-10-151-071-5

Query Match 54.0%; Score 75; DB 12; Length 443;
Best Local Similarity 52.0%; Pred. No. 0.0081;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 27
US-10-166-232A-5
Sequence 5, Application US/10166232A
Publication No. US20030021785A1
GENERAL INFORMATION:
APPLICANT: DOUGALL, William, C.
TITLE OF INVENTION: USE OF RANK ANTAGONISTS TO TREAT CANCER
FILE REFERENCE: 3278-A
CURRENT APPLICATION NUMBER: US/10/166,232A
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/296,670
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 443
TYPE: PRT
ORGANISM: Homo sapiens
US-10-166-232A-5

Query Match 54.0%; Score 75; DB 14; Length 443;
Best Local Similarity 52.0%; Pred. No. 0.0081;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 28
US-09-871-856-4
Sequence 4, Application US/09871856
Patent No. US20020081720A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM: Floppy disk

COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-871-856-4

Query Match 54.0%; Score 75; DB 9; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0083;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 29
US-09-877-650-4
Sequence 4, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM: Floppy disk

COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-877-650-4

Query Match 54.0%; Score 75; DB 9; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0083;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|||||:|:|:|:
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 30
US-09-865-363-4
; Sequence 4, Application US/09865363
; Publication No. US2002008626A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,363
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-865-363-4

Query Match 54.0%; Score 75; DB 12; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0083;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|||||:|:|:|:
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 31
US-10-405-878-4
; Sequence 4, Application US/10405878
; Publication No. US20030175840A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/405,878
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-405-878-4

Query Match 54.0%; Score 75; DB 14; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0083;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|||||:|:|:|:
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 32
US-09-871-856-2
; Sequence 2, Application US/09871856
; Patent No. US20020081720A1


```

;
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;
; US-09-871-856-2
;
; Query Match 54.0%; Score 75; DB 9; Length 591;
; Best Local Similarity 52.0%; Pred. No. 0.011;
; Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
;
; Qy 1 CRPWTNCSLDGRSVLKTGTTEKDW 25
; |||||:|:|:|:|:|
; Db 144 CRPWTNCTFLGKRVEHHGTEKSDAV 168
;
; RESULT 33
; US-09-877-650-2
; Sequence 2, Application US/09877650
; Patent No. US20020169117A1
;
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;

```

```

; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-877-650-2

Query Match          54.0%; Score 75; DB 9; Length 591;
Best Local Similarity 52.0%; Pred. No. 0.011;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      1 CRPTWNCSLDGRSVLKTGTTEKDVV 25
        |||||: |: | :| :|
DB     144 CRPTWNTCTFLGKRVEHHGTEKSDAV 168

RESULT 34
US-09-865-363-2
; Sequence 2, Application US/09865363
; Publication No. US20020086826A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
;             Galibert, Laurent
;             Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,363
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-865-363-2

Query Match          54.0%; Score 75; DB 12; Length 591;
Best Local Similarity 52.0%; Pred. NO. 0.011;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 144 CRPWTNCTFLGKRVEHHGTEKSDAV 168

RESULT 35
US-10-405-878-2
; Sequence 2, Application US/10405878
; Publication No. US20030175840A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/405,878
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

```

US-10-405-878-2

Query Match          54.0%; Score 75; DB 14; Length 591;
Best Local Similarity 52.0%; Pred. NO. 0.011;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 144 CRPWTNCTFLGKRVEHHGTEKSDAV 168

RESULT 36
US-09-871-856-6
; Sequence 6, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-871-856-6

Query Match          54.0%; Score 75; DB 9; Length 616;
Best Local Similarity 52.0%; Pred. NO. 0.012;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 37
US-09-877-650-6
; Sequence 6, Application US/09877650
; Patent No. US20020169117A1

```

```
;;
;; GENERAL INFORMATION:
;; APPLICANT: Anderson, Dirk M.
;; Galibert, Laurent
;; Maraskovsky, Eugene
;; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/877,650
;; FILING DATE: 08-Jun-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/995,659
;; FILING DATE: 1997-12-22
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2852-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 616 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-877-650-6
Query Match 54.0%; Score 75; DB 9; Length 616;
Best Local Similarity 52.0%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 9; Indels 9; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 38
US-09-865-363-6
; Sequence 6, Application US/09865363
; Publication No. US2002008626A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
;;
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/865,363
;; FILING DATE: 25-May-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/995,659
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2852-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 616 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-865-363-6
Query Match 54.0%; Score 75; DB 12; Length 616;
Best Local Similarity 52.0%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 9; Indels 9; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 39
US-10-151-071-4
; Sequence 4, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-071-4
Query Match 54.0%; Score 75; DB 12; Length 616;
Best Local Similarity 52.0%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 9; Indels 9; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

RESULT 40
US-09-957-944-2
; Sequence 2, Application US/09957944
; Publication No. US20020086312A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dougall, William C.
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVATION
; TITLE OF INVENTION: NF-kappa B
; FILE REFERENCE: 3109-A
; CURRENT APPLICATION NUMBER: US/09/957,944
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/235,157
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-944-2

Query Match      54.0%; Score 75; DB 12; Length 616;
Best Local Similarity 52.0%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
      |||||:|:|:|:|
Db      169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

Search completed: May 5, 2004, 14:53:54
Job time : 10.2466 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:41 ; Search time 2.99658 Seconds
(without alignments)
802.512 Million cell updates/sec

Title: US-10-067-122B-2_COPY_133_157
Perfect score: 139
Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	256	2 B32393	T-cell antigen 4-1
2	115	82.7	255	2 I38426	lymphocyte activat
3	73	52.5	277	2 I37552	OX40 homolog - hum
4	70	50.4	271	2 S12783	OX40 antigen precu
5	66	47.5	272	2 I48700	gene ox40 protein
6	63	45.3	277	2 A60771	B-cell activation
7	62	44.6	305	2 A46476	B cell-associated
8	53.5	38.5	772	2 D75002	chemotaxis histidi
9	50	36.0	230	2 T47317	hypothetical prote
10	50	36.0	354	2 T47965	hypothetical prote
11	49.5	35.6	170	2 E96523	hypothetical prote
12	48.5	34.9	766	2 G71160	probable histidine
13	48	34.5	115	2 AD1172	hypothetical prote
14	48	34.5	175	2 S48280	probable membrane
15	48	34.5	194	2 S57472	murine muscle LIM
16	48	34.5	194	2 A55099	muscle LIM protein
17	48	34.5	651	2 JC7705	death receptor-6 -
18	47.5	34.2	463	2 S19377	probable membrane
19	47	33.8	119	2 S75117	transposase sll198
20	47	33.8	231	2 E97280	amidase, germinati
21	47	33.8	364	2 G82740	riboflavin-specifi
22	47	33.8	998	1 QQB81	B1 protein - black
23	47	33.8	998	2 S41397	protein A - flock
24	47	33.8	1127	2 T03105	major single-stran
25	46	33.1	254	1 COBEQ2	cyclin homolog ECL
26	46	33.1	348	1 XDEC	asparaginase (EC 3
27	46	33.1	348	2 A98108	periplasmic L-aspa
28	46	33.1	348	2 D85953	periplasmic L-aspa
29	46	33.1	361	2 AF1593	B. subtilis PBSX p

30	46	33.1	494	2 A86917	probable monooxyge
31	45.5	32.7	249	2 T02123	hypothetical prote
32	45	32.4	309	1 KIFKMG	homoserine kinase
33	45	32.4	339	2 E90436	coA-ligase / coenz
34	45	32.4	358	2 AE2425	hypothetical prote
35	45	32.4	412	2 T23385	hypothetical prote
36	45	32.4	584	2 B82936	conserved hypothet
37	45	32.4	727	2 T18665	hypothetical prote
38	45	32.4	1806	2 T23298	hypothetical prote
39	44	31.7	125	2 D70732	hypothetical prote
40	44	31.7	141	2 F81433	probable heme-bind
41	44	31.7	193	2 A84479	hypothetical prote
42	44	31.7	348	2 AB0879	asparaginase (EC 3
43	44	31.7	534	2 T08414	hypothetical prote
44	44	31.7	595	2 B84906	probable calcium-d
45	44	31.7	660	2 I51684	epithelial sodium

ALIGNMENTS

RESULT 1

B32393
T-cell antigen 4-1BB precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C/Accession: B32393; I48879
R/Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A/Title: cDNA sequence of two inducible T-cell genes.
A/Reference number: A32393; MUID:89184547; PMID:2784565
A/Accession: B32393
A/Molecule type: mRNA
A/Residues: 1-256 <KWO>
A/Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
R/Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A/Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
A/Reference number: I48879; MUID:94179805; PMID:8133039
A/Accession: I48879
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-256 <RES>
A/Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C/Genetics:
A/Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Keywords: transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 100.0%; Score 139; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 3.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
|||||
DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 2

I38426
Lymphocyte activation-induced receptor ILA precursor - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C/Accession: I38426; JT0752
R/Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R
Eur. J. Immunol. 24, 2219-2227, 1994
A/Title: Molecular and biological characterization of human 4-1BB and its ligand.
A/Reference number: I38426; MUID:94374434; PMID:8088337
A/Accession: I38426
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA

A;Residues: 1-255 <RES>
A;Cross-references: EMBL:U03397; NID:G571320; PIDN:AAA53133.1; PID:G571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A;Reference number: JT0752; MUID:94085794; PMID:8262389
A;Accession: JT0752

A;Molecule type: mRNA
A;Residues: 1-106, 'R', 108-255 <SCH>
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C;Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix
C;Superfamily: glycoprotein; phosphoprotein; receptor; transmembrane protein
C;Keywords: signal sequence #status predicted <SIG>
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F;187-213/Domain: transmembrane #status predicted <TM>
F;138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDW 25
Db 133 CRPWTNCSLDGRSVLVNGTKERDW 157

RESULT 3

OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment
A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:G472957; PIDN:CAA53576.1; PID:G472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 52.5%; Score 73; DB 2; Length 277;
Best Local Similarity 40.0%; Pred. No. 0.0029;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 141 CRPWTNCTLAGKHTLOPASNSSDAI 165

RESULT 4

OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: EMBL:X17037; NID:G57830; PIDN:CAA34897.1; PID:G57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TM>

Query Match 50.4%; Score 70; DB 2; Length 271;
Best Local Similarity 40.0%; Pred. No. 0.008;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 138 CRPWTNCTLSGKQIRHPASNSLDTV 162

RESULT 5

I48700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.; H
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell inte
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:Z21674; NID:G312827; PIDN:CAA79772.1; PID:G312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-14, 'G', 16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:G732818; PIDN:CAA59476.1; PID:G732819
C;Genetics:

A;Gene: OX40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 47.5%; Score 66; DB 2; Length 272;
Best Local Similarity 40.0%; Pred. No. 0.032;
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 139 CRPWTNCTLSGKQTRHPASDSILDAV 163

RESULT 6

A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>

Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 4 WTNC--LDGRSVLKTGTTEK 22
Db 93 WTYISRFLDGRSLVKGATNK 113

RESULT 11

E96523
hypothetical protein F11A17.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: E96523
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96523
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <STO>
A;Cross-references: GB:AE005173; NID:G57333872; PIDN:AAD49760.1; GSPDB:GN00141
C;Genetics:
A;Gene: F11A17.10
A;Map position: 1
C;Superfamily: Escherichia coli ribosomal protein L18

Query Match 35.6%; Score 49.5; DB 2; Length 170;
Best Local Similarity 40.0%; Pred. No. 6;
Matches 10; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 2 RPWTNCSLDGRSVL---KTGTTEKD 23
Db 32 KPWSSSSLQSRSMVVEAKTKTSSED 56

RESULT 12

G71160
probable histidine kinase (cheA) - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: G71160
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71160
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-766 <KAW>
A;Cross-references: GB:AP000002; NID:G3236129; PIDN:BAA29572.1; PID:G3256889
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0484
C;Superfamily: chemotaxis protein cheA

Query Match 34.9%; Score 48.5; DB 2; Length 766;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 10; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 4 WTNCSLDGRSVLKTGTTEKDVV 25
Db 203 WTN---PGREIENGNGEDVV 221

RESULT 13

AD1172
hypothetical protein lmo0780 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1172
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1172
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98858.1; PID:gl6410169; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0780

Query Match 34.5%; Score 48; DB 2; Length 115;
Best Local Similarity 50.0%; Pred. No. 6.8;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 WTNCSLDGRSVLKT 17
Db 100 WAECCKQKAILKT 113

RESULT 14

S48280
probable membrane protein YBR116c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0911
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S48280; S45984; S44695
R;Mannhaupt, G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; MUID:95208357; PMID:7900426
A;Accession: S48280
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-175 <MAN>
A;Cross-references: EMBL:X78993; NID:G476045; PIDN:CAA55618.1; PID:G565057
R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
A;Accession: S45984
A;Molecule type: DNA
A;Residues: 1-175 <FE2>
A;Cross-references: EMBL:Z35985; NID:G536456; PID:G536457; MIPS:YBR116c
C;Genetics:
A;Cross-references: SGD:S0000320
A;Map position: 2R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YBR116c
C;Keywords: transmembrane protein
F;120-136/Domain: transmembrane #status predicted <TM1>
F;138-158/Domain: transmembrane #status predicted <TM2>

Query Match 34.5%; Score 48; DB 2; Length 175;
Best Local Similarity 38.1%; Pred. No. 10;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 WTNCSLDGRSVLKTGTTEKDV 24
Db 76 FTNCISQRTVLRQGLKRSI 96

```

RESULT 15
S57472
murine muscle LIM protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Jun-2001
C:Accession: S57472
R:Harrod, G.V.; Jowett, A.K.
submitted to the EMBL Data Library, June 1995
A:Description: Murine MLP: cloning and expression in the embryonic head.
A:Reference number: S57472
A:Accession: S57472
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <HAR>
A:Cross-references: EMBL:Z49883; NID:g871430; PIDN:CAA90039.1; PID:g871431
C:Superfamily: mouse muscle LIM protein MLP; LIM metal-binding repeat homology
F:10-61/Domain: LIM metal-binding repeat homology <LIM1>
F:120-171/Domain: LIM metal-binding repeat homology <LIM2>

Query Match      34.5%; Score 48; DB 2; Length 194;
Best Local Similarity 34.6%; Pred. No. 12;
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY    2 RPW-----TNCSLDGRSVLKGTGTEKD 23
      :|||          ||::||:|:|||
Db     138 KPWHKTCFRCAICGKSLESTNVTDKD 163

RESULT 16
A55099
muscle LIM protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Jun-2001
C:Accession: A55099
R:Arber, S.; Halder, G.; Caroni, P.
Cell 79, 221-231, 1994
A>Title: Muscle LIM protein, a novel essential regulator of myogenesis, promotes myogeni
A:Reference number: A55099; MUID:95042720; PMID:7954791
A:Accession: A55099
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-194 <RES>
A:Cross-references: EMBL:X81193; NID:g535068; PIDN:CAAS7065.1; PID:g535069
C:Genetics:
A:Gene: MLP
C:Superfamily: mouse muscle LIM protein MLP; LIM metal-binding repeat homology
F:10-61/Domain: LIM metal-binding repeat homology <LIM1>
F:120-171/Domain: LIM metal-binding repeat homology <LIM2>

Query Match      34.5%; Score 48; DB 2; Length 194;
Best Local Similarity 34.6%; Pred. No. 12;
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY    2 RPWTN----CSLDGRSVLKGTGTEKD 23
      :|||          ||::||:|:|||
Db     138 KPWHKTCFRCAICGKSLESTNVTDKD 163

RESULT 17
JC7705
death receptor-6 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
C:Accession: JC7705
R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A>Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A:Reference number: JC7705; MUID:21308433; PMID:11414698
A:Accession: JC7705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
A:Cross-references: GB:AF349908
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs

```

tresia, activates a cell death and/or survival signaling cascade.

C;Genetics:
A;Gene: dr-6
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: ovary

F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 34.5%; Score 48; DB 2; Length 651;
Best Local Similarity 40.0%; Pred. No. 40;
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTTEKDNV 25
 |:|:|:|:|:|:|:|:|:|:|
Db 171 CKTYTDCFGKNMVVVKPGTKESDNV 195

RESULT 18

S19377
probable membrane protein YCL048w - yeast (*Saccharomyces cerevisiae*)
C;Species: *Saccharomyces cerevisiae*
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Apr-2002
C;Accession: S19377
R;Grenson, M.; Jauniaux, J.C.; Urrestarazu, L.A.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19376
A;Accession: S19377
A;Molecule type: DNA
A;Residues: 1-463 <GRE>
A;Cross-references: EMBL:X59720; NID:g1907116; PID:g5313; GSPDB:GN00003; MIPS:YCL048w
C;Genetics:
A;Gene: MIPS:YCL048w
A;Cross-references: SGD:S0000553
A;Map position: 3L
C;Keywords: transmembrane protein
F;7-29/Domain: transmembrane #status predicted <TM1>
F;446-463/Domain: transmembrane #status predicted <TM2>

Query Match 34.2%; Score 47.5; DB 2; Length 463;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 CRPWTNCSLDGRSVLKTG 18
 |||||:|:|:|:|:|:|
Db 378 CNKWTNPS-NGRSIRGG 394

RESULT 19

S75117
transposase sll1985 - *Synechocystis* sp. (strain PCC 6803)
N;Alternate names: protein sll1985
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 15-Oct-1999
C;Accession: S75117
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75117
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-119 <KAN>
A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17979.1; PID:d101871;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Keywords: DNA binding; DNA recombination

Query Match 33.8%; Score 47; DB 2; Length 119;

Best Local Similarity 50.0%; Pred. No. 9.9;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 RPWTNCSLDGRSVLKT 17
||| | :||: |
Db 104 RPWNQKVDGKTYLTT 119

RESULT 20
E97280
amidase, germination specific (cwlc/cwld B. subtilis ortholog) [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: E97280
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E97280
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81032.1; PID:g15026157; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3092

Query Match 33.8%; Score 47; DB 2; Length 231;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTEKDV 24
:|: | | | | |
Db 50 IDGGANLKDGTEKDI 65

RESULT 21
G82740
riboflavin-specific deaminase XF0950 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: G82740
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82740
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <SIM>
A;Cross-references: GB:AE003934; GB:AE003849; NID:g9105876; PIDN:AAF83760.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0950
C;Superfamily: Chlamydomphila pneumoniae riboflavin-specific deaminase

Query Match 33.8%; Score 47; DB 2; Length 364;

Best Local Similarity 41.7%; Pred. No. 31;
Matches 10; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 2 RPWT---NCSLDGRSVLKTGTTT 21
||| | :||: |
Db 151 RPWVRIKLGSSLDGRTALASGESK 174

RESULT 22
Q0BBB1
B1 protein - black beetle virus
C;Species: black beetle virus
C;Date: 30-Sep-1992 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: S78471; S28728; S28729; A23243
R;Dasgupta, R.
submitted to the EMBL Data Library, July 1986
A;Reference number: S78471
A;Accession: S78471
A;Molecule type: genomic RNA
A;Residues: 1-998 <DAS>
A;Cross-references: EMBL:X02396; NID:g60679; PIDN:CAA26238.1; PID:g60680
R;Dasmahapatra, B.; Dasgupta, R.; Ghosh, A.; Kaesberg, P.
J. Mol. Biol. 182, 183-189, 1985
A;Title: Structure of the black beetle virus genome and its functional implications.
A;Reference number: S28728; MUID:85210903; PMID:3839022
A;Accession: S28728
A;Molecule type: genomic RNA
A;Residues: 1-883, 'AALRTPWTNRYQC' <DAW>
A;Cross-references: EMBL:X02396
A;Accession: S28729
A;Molecule type: genomic RNA
A;Residues: 897-998 <DA2>
A;Cross-references: EMBL:X02396
R;Guarino, L.A.; Ghosh, A.; Dasmahapatra, B.; Dasgupta, R.; Kaesberg, P.
Virology 139, 199-203, 1984
A;Title: Sequence of the black beetle virus subgenomic RNA and its location in the viral
A;Reference number: A23243; MUID:85042104; PMID:6495657
A;Accession: A23243
A;Molecule type: genomic RNA
A;Residues: 897-998 <GUA>
A;Cross-references: GB:M33065; NID:g210673; PIDN:AAA42745.1; PID:g210674
C;Superfamily: black beetle virus B1 protein
C;Keywords: RNA biosynthesis

Query Match 33.8%; Score 47; DB 1; Length 998;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7
||| | |
Db 262 CRPWTDC 268

RESULT 23
S41397
protein A - flock house virus
C;Species: flock house virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
C;Accession: S41397
R;Dasgupta, R.
submitted to the EMBL Data Library, January 1994
A;Description: Near identity in the polymerase gene of two serologically distinct nodavin
A;Reference number: S41397
A;Accession: S41397
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-998 <DAS>
A;Cross-references: EMBL:X77156; NID:g450500; PIDN:CAA54399.1; PID:g450501
C;Superfamily: black beetle virus B1 protein

Query Match 33.8%; Score 47; DB 2; Length 998;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7
Db 262 CRPWTDC 268

RESULT 24
T03105
major single-stranded DNA binding protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C;Accession: T03105
R;Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: Z14840; MUID:97404659; PMID:9261371
A;Accession: T03105
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1127 <ENS>
A;Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58057.1; PID:g2337973
C;Superfamily: herpesvirus DNA-binding protein
C;Keywords: DNA binding

Query Match 33.8%; Score 47; DB 2; Length 1127;
Best Local Similarity 52.2%; Pred. No. 1e+02;
Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 3 PWTNCSLDGRSVLKTGTTEKDV 25
Db 1069 PWTHEWAE--SVLKSGTCETDEV 1089

RESULT 25
COBEQ2
cyclin homolog ECLF2 - saimirine herpesvirus 1 (strain 11)
C;Species: saimirine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: S20243; F36813
R;Nicholas, J.; Cameron, K.R.; Honess, R.W.
Nature 355, 362-365, 1992
A;Title: Herpesvirus saimiri encodes homologues of G protein-coupled receptors and cyclin
A;Reference number: S20243; MUID:92115001; PMID:1309943
A;Accession: S20243
A;Molecule type: DNA
A;Residues: 1-254 <NIC>
A;Cross-references: GB:S76368; NID:g2433351; PIDN:AAB21115.1; PID:g2433352
R;Albrecht, J.
submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A36806
A;Accession: F36813
A;Molecule type: DNA
A;Residues: 1-254 <ALB>
A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45695.1; PID:g60393
R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Wi
J. Virol. 66, 5047-5058, 1992
A;Title: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A37309; MUID:92333688; PMID:1321287
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
C;Genetics:
A;Gene: ECLF2; 72
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 33.1%; Score 46; DB 1; Length 254;
Best Local Similarity 44.8%; Pred. No. 31;
Matches 13; Conservative 1; Mismatches 11; Indels 4; Gaps 1;

QY 1 CRPWTNCSLDGRSVLKTGT-----TEKDVV 25
Db 1069 PWTHEWAE--SVLKSGTCETDEV 1089

Db 214 CRPWTCTYLEDLSSILNFSNTVTRTVKDV 242

RESULT 26
XDEC
asparaginase (EC 3.5.1.1) II precursor [validated] - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1990 #text_change 01-Mar-2002
C;Accession: A35132; JU0301; A01000; D65081
R;Jennings, M.P.; Beacham, I.R.
J. Bacteriol. 172, 1491-1498, 1990
A;Title: Analysis of the Escherichia coli gene encoding L-asparaginase II, ansB, and its
A;Reference number: A35132; MUID:90170867; PMID:2407723
A;Accession: A35132
A;Molecule type: DNA
A;Residues: 1-348 <JEN>
A;Cross-references: EMBL:X52540
R;Bonthron, D.T.
Gene 91, 101-105, 1990
A;Title: L-Asparaginase II of Escherichia coli K-12: cloning, mapping and sequencing of t
A;Reference number: JU0301; MUID:90382683; PMID:2144836
A;Accession: JU0301
A;Molecule type: DNA
A;Residues: 1-348 <BON>
A;Cross-references: GB:M34234; NID:g145276; PIDN:AAA23445.1; PID:g145277
A;Experimental source: strain K12 JM108
R;Maita, T.; Matsuda, G.
Hoppe-Seyler's Z. Physiol. Chem. 361, 105-117, 1980
A;Title: The primary structure of L-asparaginase from Escherichia coli.
A;Reference number: A01000; MUID:80135739; PMID:6766894
A;Accession: A01000
A;Molecule type: protein
A;Residues: 23-48, 'A', 50-85, 'D', 87-131, 133-155, 157-170, 172-205, 'D', 207-267, 'D', 269-273, 'J
R;Peterson, R.G.; Richards, F.F.; Handschumacher, R.E.
J. Biol. Chem. 252, 2072-2076, 1977
A;Title: Structure of peptide from active site region of Escherichia coli L-asparaginase
A;Reference number: A32655; MUID:77140944; PMID:321449
A;Contents: annotation; active site
R;Greenquist, A.C.; Wriston Jr., J.C.
Arch. Biochem. Biophys. 152, 280-286, 1972
A;Title: Chemical evidence for identical subunits in L-asparaginase from Escherichia coli
A;Reference number: A37451; MUID:73007901; PMID:4561256
A;Contents: annotation
A;Note: the cysteine residues were quantitated and shown to form intrachain bonds
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D65081
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-348 <BLAT>
A;Cross-references: GB:AF000378; GB:U00096; NID:g1789319; PIDN:AAC75994.1; PID:g1789327;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ansB
A;Map position: 64 min
C;Complex: homotetramer
C;Function:
A;Description: EC 3.5.1.1 [validated, MUID:90170867]; catalyzes the hydrolysis of aspara
A;Note: has a higher affinity for asparagine than asparaginase I (PIR:XDEC1)
A;Note: positively regulated by cAMP receptor protein (CRP) (PIR:QRECC) and by FNR protei
C;Superfamily: asparaginase
C;Keywords: extracellular protein; homotetramer; hydrolase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-348/Product: asparaginase #status experimental <MAT>
F;99-127/Disulfide bonds: #status experimental
F;142/Active site: Ser #status experimental

Query Match 33.1%; Score 46; DB 1; Length 348;
Best Local Similarity 69.2%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTE 21
|||||
Db 177 LDGRDVTKTNTTD 189

RESULT 27

A; periplasmic L-asparaginase II [imported] - Escherichia coli (strain O157:H7, substrain R
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C; Accession: A98108
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: A98108
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-348 <HAY>
A; Cross-references: GB:BA000007; PIDN:BA037256.1; PID:gl13363305; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: ECS3833
C; Superfamily: asparaginase

Query Match 33.1%; Score 46; DB 2; Length 348;
Best Local Similarity 69.2%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTE 21
|||||
Db 177 LDGRDVTKTNTTD 189

RESULT 28

D85953
periplasmic L-asparaginase II [imported] - Escherichia coli (strain O157:H7, substrain H
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: D85953
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: D85953
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-348 <STO>
A; Cross-references: GB:AE005174; NID:gl2517506; PIDN:AAG58088.1; GSPDB:GN00145; UWGP:243
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: ansB
C; Superfamily: asparaginase

Query Match 33.1%; Score 46; DB 2; Length 348;
Best Local Similarity 69.2%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTE 21
|||||
Db 177 LDGRDVTKTNTTD 189

RESULT 29

AF1593
B. subtilis PBSX prophage protein homolog lin1287 [imported] - Listeria innocua (strain
C; Species: Listeria innocua
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C; Accession: AF1593
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AF1593
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-361 <GLA>
A; Cross-references: GB:AL592022; PIDN:CAC96518.1; PID:gl16413760; GSPDB:GN00178
A; Experimental source: strain Clp11262
C; Genetics:
A; Gene: lin1287

Query Match 33.1%; Score 46; DB 2; Length 361;
Best Local Similarity 36.4%; Pred. No. 44;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 WTNCSLDGRSVLKTGTTEKDVV 25
|||||
Db 268 WKTINISGLVLKDKGSVNDVI 289

RESULT 30

A86917
probable monooxygenase [imported] - Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Accession: A86917
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A; Title: Massive gene decay in the leprosy bacillus.
A; Reference number: A86909; MUID:21128732; PMID:11234002
A; Accession: A86917
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-494 <STO>
A; Cross-references: GB:AL450380; NID:gl3092457; PIDN:CAC29573.1; GSPDB:GN00147
C; Genetics:
A; Gene: ML0065

Query Match 33.1%; Score 46; DB 2; Length 494;
Best Local Similarity 47.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 RPWTNCS--LDGRSVLK 16
|||||
Db 72 RPWTKCQAIDGKPILE 88

RESULT 31

T02123
hypothetical protein At2g40960 [imported] - Arabidopsis thaliana
N; Alternate names: hypothetical protein T20B5.16; hypothetical protein T3K9.27
C; Species: Arabidopsis thaliana (mouse-ear cross)
C; Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 02-Feb-2001
C; Accession: T00760; T02123; A84836
R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, November 1997
A; Description: Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence.
A; Reference number: Z14159
A; Accession: T00760

A; Status: translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-249 <ROU>
A; Cross-references: EMBL:AC002409; NID:g2623294; PID:g2623310
A; Experimental source: cultivar Columbia
R; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: F81433
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <PAR>
A;Cross-references: GB:AL1139074; GB:AL111168; NID:G6967505; PIDN:CAB72642.1; PID:G696769
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0158c
C;Superfamily: Campylobacter jejuni probable heme-binding lipoprotein Cj0158c
Query Match 31.7%; Score 44; DB 2; Length 141;
Best Local Similarity 42.1%; Pred. No. 33;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 7 CSLDGRSVLKTGTTEKDVV 25
|||:::|:::|
Db 20 CSNDEKNISKNTQNTDQEVV 38

Search completed: May 5, 2004, 14:41:22
Job time : 3.99658 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:56 ; Search time 1.96918 Seconds
(without alignments)
661.065 Million cell updates/sec

Title: US-10-067-122B-2_COPY_133_157
Perfect score: 139
Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	139	100.0	256	1	TNR9_MOUSE	P20334 mus musculu
2	115	82.7	255	1	TNR9_HUMAN	Q07011 homo sapien
3	86	61.9	625	1	TR11_MOUSE	O35305 mus musculu
4	75	54.0	616	1	TR11_HUMAN	Q3y6q6 homo sapien
5	73	52.5	277	1	TNR4_HUMAN	P43489 homo sapien
6	70	50.4	271	1	TNR4_RAT	P15725 rattus norv
7	66	47.5	272	1	TNR4_MOUSE	P47741 mus musculu
8	63	45.3	277	1	TNR5_HUMAN	P25942 homo sapien
9	62	44.6	289	1	TNR5_MOUSE	P27512 mus musculu
10	53.5	38.5	1179	1	EX5B_BUCAP	Q8k9a9 buchnera ap
11	52	37.4	269	1	TNR5_BOVIN	Q28203 bos taurus
12	50	36.0	655	1	TR21_HUMAN	O75509 homo sapien
13	49	35.3	430	1	TRLT_MACFA	Q9n092 macaca fasc
14	48	34.5	175	1	YBW6_YEAST	P38268 saccharomyc
15	48	34.5	194	1	CSR3_HUMAN	P50461 homo sapien
16	48	34.5	194	1	CSR3_MOUSE	P50462 mus musculu
17	48	34.5	194	1	CSR3_RAT	P50463 rattus norv
18	48	34.5	228	1	TR18_MOUSE	O35714 mus musculu
19	47.5	34.2	463	1	YCE8_YEAST	P25380 saccharomyc
20	47	33.8	415	1	TNR3_MOUSE	P50284 mus musculu
21	47	33.8	998	1	RRPO_BBV	Q96631 black beetl
22	47	33.8	998	1	RRPO_BOOLV	Q992j0 boolarra vi
23	47	33.8	998	1	RRPO_FHV	Q86929 flock house
24	46	33.1	241	1	TR18_HUMAN	Q9y5u5 homo sapien
25	46	33.1	254	1	CGH2_HSVSA	Q01043 herpesvirus
26	46	33.1	348	1	ASG2_ECOLI	P08005 escherichia
27	45	32.4	308	1	KHSE_CORGL	P07128 corynebacte
28	45	32.4	401	1	T11B_HUMAN	O00300 homo sapien
29	45	32.4	401	1	T11B_RAT	O08727 rattus norv
30	45	32.4	412	1	RBA1_CAEEL	P90917 caenorhabdi
31	45	32.4	655	1	TR21_MOUSE	Q9epu5 mus musculu
32	44	31.7	125	1	YM88_MYCTU	Q50677 mycobacteri
33	44	31.7	357	1	WN9B_HUMAN	O14905 homo sapien

ALIGNMENTS

RESULT 1

ID	TNR9_MOUSE	STANDARD;	PRT;	256 AA.
AC	P20334;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB			
DE	ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).			
GN	TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89184547; PubMed=2784565;			
RA	Kwon B.S., Weissman S.M.;			
RT	"cDNA sequences of two inducible T-cell genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	MEDLINE=94179805; PubMed=8133039;			
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;			
RT	"Genomic organization and chromosomal localization of the T-cell			
RT	antigen 4-1BB.";			
RL	J. Immunol. 152:2256-2262(1994).			
RN	[3]			
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.			
RX	MEDLINE=93139510; PubMed=7678621;			
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,			
RA	Kwon B.S.;			
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and			
RT	function.";			
RL	J. Immunol. 150:771-781(1993).			
CC	-!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T			
CC	cell activation.			
CC	-!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.			
CC	ASSOCIATES WITH P56-LCK. Interacts with TRAF1, TRAF2 AND TRAF3 (By			
CC	similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.			
CC	-!- INDUCTION: Optimal by PMA and ionomycin.			
CC	-!- SIMILARITY: Contains 4 TNFR-Cys repeats.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J04492; AAA40167.1; -.			
DR	EMBL; U02567; AAA93113.1; -.			

DR PIR; B32393; B32393.
DR PDB; 1D0J; 26-SEP-01.
DR MGI; 1101059; Tnfrsf9.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 256
FT DOMAIN 25 187
FT TRANSMEM 188 208
FT DOMAIN 209 256
FT REPEAT 17 45
FT REPEAT 46 85
FT REPEAT 86 117
FT REPEAT 118 159
FT DISULFID 28 37
FT DISULFID 31 44
FT DISULFID 47 61
FT DISULFID 64 77
FT DISULFID 67 85
FT DISULFID 87 93
FT DISULFID 98 105
FT DISULFID 101 116
FT DISULFID 119 133
FT DISULFID 139 158
FT CARBOHYD 128 128
FT CARBOHYD 138 138
SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.8e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDW 25
|||||
Db 133 CRPWTNCSLDGRSVLKTGTTEKDW 157

RESULT 2
TNR9 HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA) (CD137 antigen).
DE TNFRSF9 OR ILA OR CD137.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its ligand."
RT Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor

RT family.";
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;
RT "Characterization of human homologue of 4-1BB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Pearce A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
RX MEDLINE=98078711; PubMed=9418902;
RA Arch R.H., Thompson C.B.;
RT "4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB.";
RL Mol. Cell. Biol. 18:558-565(1998).
RN [8]
RP INTERACTION WITH TRAF1 AND TRAF2.
RX MEDLINE=98270914; PubMed=9607925;
RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A., Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y., Watts T.H.;
RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by 4-1BB ligand.";
RL J. Exp. Med. 187:1849-1862(1998).
RN [9]
RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
RX MEDLINE=21662677; PubMed=11804328;
RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in 4-1BB-mediated signal transduction.";
RL Mol. Cells 12:304-312(2001).
CC -1- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.
CC -1- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with LRR-repeat protein 1/LRR-1.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.

DR Pfam; PF00020; TNFR_C6; 3.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00500; TNFR_NGFR_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 625 TUMOR NECROSIS FACTOR RECEPTOR
 FT DOMAIN 31 214 SUPERFAMILY MEMBER 11A.
 FT TRANSMEM 215 234 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 235 625 POTENTIAL.
 FT REPEAT 35 69 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 72 113 TNFR-CYS 1.
 FT REPEAT 115 152 TNFR-CYS 2.
 FT REPEAT 155 195 TNFR-CYS 3.
 FT REPEAT 35 47 TNFR-CYS 4.
 FT DISULFID 48 61 BY SIMILARITY.
 FT DISULFID 51 69 BY SIMILARITY.
 FT DISULFID 72 87 BY SIMILARITY.
 FT DISULFID 93 113 BY SIMILARITY.
 FT DISULFID 115 128 BY SIMILARITY.
 FT DISULFID 134 152 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 494 494 R -> K (IN REF. 2).
 SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;

Query Match 61.9%; Score 86; DB 1; Length 625;
 Best Local Similarity 60.0%; Pred. No. 2.4e-05;

Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDW 25

Db 170 CKPWTNCTLLGKLEAHQGTESDV 194

RESULT 4

TR11 HUMAN STANDARD; PRT; 616 AA.
 ID TR11_HUMAN STANDARD; PRT; 616 AA.
 AC Q9Y6Q6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11A precursor
 DE (Receptor activator of NF-KB) (Osteoclast differentiation factor
 DE receptor) (ODF).
 DE TNFRSF11A OR RANK.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Dendritic cell;
 RX MEDLINE=98032977; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
 RA Galibert L.;
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [2]
 RN FUNCTION.
 RP MEDLINE=99097247; PubMed=9878548;
 RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
 RA Morinaga T., Higashio K.;
 RT "RANK is the essential signaling receptor for osteoclast
 RL differentiation factor in osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
 RN [3]
 RP INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.
 RX MEDLINE=98447691; PubMed=9774460;
 RA Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steinman R.M.,

RA Choi Y.;
 RT "The TRAF family of signal transducers mediates NF-kappaB activation
 RT by the TRANCE receptor.";
 RL J. Biol. Chem. 273:28355-28359(1998).
 RN [4]
 RP VARIANT FEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2
 RP ALA-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.
 RX MEDLINE=20082806; PubMed=10615125;
 RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
 RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
 RA Anderson D.M.;
 RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
 RT familial expansile osteolysis.";
 RL Nat. Genet. 24:45-48(2000).
 CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANSC/OPGL; essential for
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
 CC interactions between T-cells and dendritic cells.
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
 CC skeletal muscle, thymus, liver, colon, small intestine and adrenal
 CC gland.
 CC -!- DISEASE: Defects in TNFRSF11A are the cause of familial expansile
 CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant
 CC bone disorder characterized by focal areas of increased bone
 CC remodelling. The osteolytic lesions develop usually in the long
 CC bones during early adulthood. FEO is often associated with early
 CC onset deafness and loss of dentition.
 CC -!- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone
 CC 2 (PDB2) [MIM:602080]; also known as familial Paget disease of
 CC bone. PDB2 is a bone remodelling disorder with clinical
 CC similarities to FEO. Unlike FEO, however, affected individuals
 CC have involvement of the axial skeleton with lesions in the spine,
 CC pelvis and skull.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AF018253; AAB86809.1; -.
 CC HSSP; P25942; 1CDF.
 CC Genew; HGNC:11908; TNFRSF11A.
 CC MIM; 603499; -.
 CC MIM; 174810; -.
 CC MIM; 602080; -.
 CC GO; GO:0004872; F:receptor activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 4.
 CC SMART; SM00208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; 1.
 CC PROSITE; PS00500; TNFR_NGFR_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
 KW Disease mutation; Deafness.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR
 FT DOMAIN 30 212 SUPERFAMILY MEMBER 11A.
 FT TRANSMEM 213 233 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 234 616 POTENTIAL.
 FT REPEAT 34 68 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 71 112 TNFR-CYS 1.
 FT REPEAT 114 151 TNFR-CYS 2.
 FT REPEAT 154 194 TNFR-CYS 3.
 FT DISULFID 34 46 TNFR-CYS 4.
 FT DISULFID 47 60 BY SIMILARITY.

```
FT DISULFID 50 68 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 92 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 133 151 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 21 21 L -> LALLLCALL (in PDB2).
FT VARIANT 21 21 /FTID=VAR 011516.
FT VARIANT 192 192 L -> LLLCALL (in FEO).
FT VARIANT 192 192 /FTID=VAR 011517.
FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;
Query Match 54.0%; Score 75; DB 1; Length 616;
Best Local Similarity 52.0%; Pred. No. 0.0012;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVHEHGTESDAV 193

RESULT 5
TNR4_HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE receptor) (ACT35 antigen) (TAX-transcriptionally activated
DE glycoprotein 1 receptor) (CD134 antigen).
DE TNFRSF4 OR TXGPIL.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homolog: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen.";
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95219871; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Seidin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor.";
RL Circ. Shock 44:30-34(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318724; PubMed=10861060;
RA Pankow R., Duerkop H., Latza U., Krause H., Kunzendorf U., Pohl T.,
RA Bulfone-Paus S.;
RT "The HTLV-I protein transcriptionally modulates OX40 antigen
RT expression.";
RL J. Immunol. 165:263-270(2000).
RN [4]
RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
RX MEDLINE=98078711; PubMed=9418902;
RA Arch R.H., Thompson C.B.;
RT "4-1BB and OX40 are members of a tumor necrosis factor (TNF)-nerve
RT growth factor receptor subfamily that bind TNF receptor-associated
RT factors and activate nuclear factor kappaB.";
RL Mol. Cell. Biol. 18:558-565(1998).
RN [5]
RP INTERACTION WITH TRAF2 AND TRAF5.
```

```
RX MEDLINE=98157982; PubMed=9488716;
RA Kawamata S., Hori T., Imura A., Takaori-Kondo A., Uchiyama T.;
RT "Activation of OX40 signal transduction pathways leads to tumor
RT necrosis factor receptor-associated factor (TRAF) 2- and
RT TRAF5-mediated NF-kappaB activation.";
RL J. Biol. Chem. 273:5808-5814(1998).
CC -!- FUNCTION: Receptor for TNFSF4/OX40L/GP34.
CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X75962; CAA53576.1; -
DR EMBL; S76792; AAB33944.1; ALT INIT.
DR EMBL; AJ277151; CAB96543.1; -
DR PIR; I37552; I37552.
DR HSSP; O14763; 1D0G.
DR Genew; HGNC:11918; TNFRSF4.
DR MIM; 600315; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005027; F: NGF/TNF (6 C-domain) receptor activity; TAS.
DR GO; GO:0006955; P: immune response; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 277 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 4.
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 235 POTENTIAL.
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
FT REPEAT 30 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 127 167 TNFR-CYS 4.
FT DISULFID 31 42 BY SIMILARITY.
FT DISULFID 43 56 BY SIMILARITY.
FT DISULFID 46 64 BY SIMILARITY.
FT DISULFID 67 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 87 107 BY SIMILARITY.
FT DISULFID 109 125 BY SIMILARITY.
FT DISULFID 128 141 BY SIMILARITY.
FT DISULFID 147 166 BY SIMILARITY.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 52.5%; Score 73; DB 1; Length 277;
Best Local Similarity 40.0%; Pred. No. 0.00097;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 141 CKPWTNCTLAGKHTLQPASNSSDAI 165

RESULT 6
TNR4_RAT
ID TNR4_RAT
AC P15725; STANDARD; PRT; 271 AA.
```


FT DISULFID 126 139 BY SIMILARITY.
FT DISULFID 145 164 BY SIMILARITY.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 47.5%; Score 66; DB 1; Length 272;
Best Local Similarity 40.0%; Pred. No. 0.011;
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRPTWCSLDGRSVLKTGTTEKDVV 25
|:|||||:|:
Db 139 CKPWNTCLSGKQTRHPASDLSLDAV 163

RESULT 8
TNR5_HUMAN STANDARD; PRT; 277 AA.
AC P25942; Q9BYU0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
RA Lehaeslaihio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=21117110; PubMed=11172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

RN [4]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
RN [6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216;
RA Sato T., Irie S., Reed J.C.;
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40.";
RL FEBS Lett. 358:113-118(1995).
RN [7]
RP INTERACTION WITH TRAF1; TRAF2; TRAF3 AND TRAF5.
RX MEDLINE=98384149; PubMed=9718306;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
RA Kehry M.R.;
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
RT interactions: regulation of CD40 signaling through multiple TRAF
RT binding sites and TRAF hetero-oligomerization.";
RL Biochemistry 37:11836-11845(1998).
RN [8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
RN [9]
RP INTERACTION WITH TRAF6.
RX MEDLINE=98095703; PubMed=9432981;
RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,
RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.;
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
RT extracellular signal-regulated kinase (ERK) activity in CD40
RT signaling along a ras-independent pathway.";
RL J. Exp. Med. 187:237-244(1998).
RN [10]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajcath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [11]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;

RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.,
RT "The role of polar interactions in the molecular recognition of CD40L
RL with its receptor CD40.",
RN Protein Sci. 7:1124-1135(1998).
RP [12]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=20442386; PubMed=10984535;
RA Ni C.Z., Welsh K., Leo E., Chion C.K., Wu H., Reed J.C., Ely K.R.,
RT "Molecular basis for CD40 signaling mediated by TRAF3.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=22000222; PubMed=12005438;
RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
RT Satterthwait A.C., Cheng G., Ely K.R.,
RA "Downstream regulator TANK binds to the CD40 recognition site on
RT TRAF3.",
RL Structure 10:403-411(2002).
RN [14]
RP VARIANT HIGM3 ARG-83.
RX MEDLINE=21532985; PubMed=11675497;
RA Ferrarri S., Giliani S., Insalaco A., Al-Ghonaïm A., Soresina A.R.,
RA Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,
RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
RA Plebani A.,
RT "Mutations of CD40 gene cause an autosomal recessive form of
RT immunodeficiency with hyper IgM.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
CC secreted (isoform II).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=P25942-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P25942-2; Sequence=VSP_006472, VSP_006473;
CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
CC -!- DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM
CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an
CC autosomal recessive disorder which includes an inability of B
CC cells to undergo isotype switching, one of the final
CC differentiation steps in the humoral immune system, an inability
CC to mount an antibody-specific immune response, and a lack of
CC germinal center formation.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAMB=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X60592; CAA43045.1; -.
CC EMBL; AL035662; CAC17670.1; -.
CC EMBL; AJ300189; CAC29424.1; -.
CC EMBL; BC012419; AAH12419.1; -.
CC PIR; S04460; A60771.
CC PDB; 1CDF; 01-APR-97.
CC PDB; 1FLL; 18-OCT-00.
CC PDB; 1LOA; 08-FEB-00.
CC PDB; 1CZZ; 26-SEP-01.

Query Match

45.3%; Score 63; DB 1; Length 277;

Best Local Similarity 44.0%; Pred. No. 0.033;
Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 161 CHPTWTCETKDLVVQAGTKNTDVV 185
RESULT 9
TNR5_MOUSE
ID TNR5_MOUSE STANDARD; PRT; 289 AA.
AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.,
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.",
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BAUB/c;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC STRAIN=BAUB/c; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.,
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.",
RL J. Immunol. 149:3921-3926(1992).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND
RP V).
RX MEDLINE=21117110; PubMed=11172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.,
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.,
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.",
RL Science 267:1494-1498(1995).
RN [6]
RP INTERACTION WITH TRAF5.
RX MEDLINE=96382484; PubMed=8790348;
RA Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,
RA Yamamoto T., Inoue J.-I.,
RT "TRAF5, a novel tumor necrosis factor receptor-associated factor
RT family protein, mediates CD40 signaling.",
RL Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,
CC TRAF2 and TRAF6 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV
CC and V); secreted (isoform II).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=I;
CC IsoId=P27512-1; Sequence=Displayed;


```
CC Name=II;
CC IsoId=P27512-2; Sequence=VSP_006474, VSP_006475;
CC Name=III;
CC IsoId=P27512-3; Sequence=VSP_006477, VSP_006478;
CC Name=IV;
CC IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
CC Name=V;
CC IsoId=P27512-5; Sequence=VSP_006476;
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M83312; AAB08705.1; -.
CC EMBL; M94126; AAA37404.1; -.
CC EMBL; M94129; AAA37404.1; JOINED.
CC EMBL; M94128; AAA37404.1; JOINED.
CC EMBL; M94127; AAA37404.1; JOINED.
CC EMBL; AJ401387; CAC29427.1; -.
CC EMBL; AJ401388; CAC29428.1; -.
CC EMBL; AJ401389; CAC29429.1; -.
CC EMBL; AJ401390; CAC29430.1; -.
CC PIR; A46476; A46476.
CC HSSP; P25942; 1CDF.
CC MGD; MGI:88336; Tnfrsf5.
CC InterPro; IPR008063; Fas receptor.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00500; TNFR_NGFR_2; 4.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
CC Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 289
FT -----
FT DOMAIN 20 193
FT TRANSMEM 194 215
FT DOMAIN 216 289
FT REPEAT 25 60
FT REPEAT 61 103
FT REPEAT 104 144
FT REPEAT 145 187
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153
FT VARSPLIC 166
FT -----
FT VARSPLIC 204 289
FT VARSPLIC 187 216
FT VARSPLIC 216 234
FT VARSPLIC 235 289
FT VARSPLIC 216 222
```

```
FT VARSPLIC 223 289
FT Missing (in isoform IV).
FT /FTid=VSP_006480.
SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match 44.6%; Score 52; DB 1; Length 289;
Best Local Similarity 40.0%; Pred. No. 0.049;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 161 CYPWTSCEBKNLEVLQKTSQTNVI 185

RESULT 10
EXSB_BUCAP
ID EXSB_BUCAP STANDARD; PRT; 1179 AA.
AC Q8K9A9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
GN RECB OR BUSG439.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -!- FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE
CC UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-
CC STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION. ALL OF
CC THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of
CC ATP) in either 5'- to 3'- or 3'- to 5'-direction to yield 5'-
CC phosphooligonucleotides.
CC -!- SUBUNIT: Consist of three subunits; recB, recC and recD (By
CC similarity).
CC -!- SIMILARITY: Belongs to the helicase family. UvrD subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE014120; AAM67982.1; -.
CC InterPro; IPR004586; RecB.
CC InterPro; IPR000212; UvrD-helicase.
CC Pfam; PF00580; UvrD-helicase; 1.
CC TIGRFAMS; TIGR00609; recB; 1.
KW Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
KW DNA repair; Complete proteome.
FT NP_BIND 39 46
FT SEQUENCE 1179 AA; 141040 MW; FECECG60F11420937 CRC64;

Query Match 38.5%; Score 53.5; DB 1; Length 1179;
Best Local Similarity 37.0%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 7; Indels 5; Gaps 1;
```

```
QY 4 WTNCSLDGRSVLKTGT-----TEKDVV 25
Db 538 WLTCSKKGAIISDGSQERILTEKDIV 564
```

```
RESULT 11
TNRS_BOVIN
ID TNRS_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U57745; AAC48710.1; -.
CC HSSP; P25942; 1CDF.
CC InterPro; IPR008063; Fas receptor.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 4.
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00050; TNFR_NGFR_2; 1.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 >269
FT
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 5.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215
FT DOMAIN 20 193
FT TRANSMEM 194 215
FT DOMAIN 216 >269
FT REPEAT 25 60
FT REPEAT 61 103
FT REPEAT 104 144
FT REPEAT 145 187
FT REPEAT 145 187
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT DISULFID 153 153
FT CARBOHYD 180 180
FT CARBOHYD 269 269
FT NON_TER
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match 37.4%; Score 52; DB 1; Length 269;
Best Local Similarity 40.0%; Pred. No. 1.5;
Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

OY 1 CRPWTNCSLDGRSVLKTGTTTEKDVV 25
Db 161.CHRWTSCEKGLVEQHVGTNKTDDV 185

RESULT 12
TR21_HUMAN
ID TR21_HUMAN STANDARD; PRT; 655 AA.
AC O75509; Q96D86;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98378343; PubMed=9714541;
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C.,
RA Aggarwal B.B., Ni J., Dixit V.M.;
RT "Identification and functional characterization of DR6, a novel death
RT domain-containing TNF receptor.";
RL FEBS Lett. 431:351-356(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC -!- SUBUNIT: Associates with TRADD.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta,
CC pancreas, lymph node, thymus and prostate. Detected at lower
CC levels in lung, skeletal muscle, kidney, testis, uterus, small
CC intestine, colon, spleen, bone marrow and fetal liver. Very low
CC levels were found in adult liver and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
```


CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X78993; CAA55618.1; -;
DR EMBL; Z35985; CAA85073.1; -;
DR PIR; S48280; S48280.
DR GexmOnline; 138659; -;
DR SGD; S0000320; YBR116C.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 143 166 POTENTIAL.
SQ SEQUENCE 175 AA; 20215 MW; 6CF72CC0909E055E CRC64;

Query Match 34.5%; Score 48; DB 1; Length 175;
Best Local Similarity 38.1%; Pred. No. 3.9;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 4 WTNCSLDGRSVLKTGTTEKDV 24
Db 76 FTNCISQRTVLRQGLXRSI 96

RESULT 15

CSR3 HUMAN STANDARD; PRT; 194 AA.
AC P50461; Q9P131;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE LIM domain protein, cardiac (Muscle LIM protein) (Cysteine-rich
DE protein 3) (CRP3).
GN CSR3 OR CLP OR MLP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=96039282; PubMed=7490106;
RA Fung Y.W., Wang R.X., Heng H.H.Q., Liew C.C.;
RT "Mapping of a human LIM protein (CLP) to human chromosome 11p15.1 by
RT fluorescence in situ hybridization.";
RL Genomics 28:602-603(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Medvedev A., Jettten A.M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yasunaga S., Harada H., Kimura A.;
RT "Cloning and characterization of the human muscle LIM protein gene.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Chen K.H., Zhang J.F., Ma D.L., Tang J.;
RT "A novel member of LIM gene family involved in cardiovascular
RT diseases.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Testis;
RX MEDLINE=22388257; PubMed12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP VARIANT CMDIM ARG-4.
RX MEDLINE=22395799; PubMed=12507422;
RA Kneoll R., Hoshijima M., Hoffman H.M., Person V., Lorenzen-Schmidt I.,
RA Bang M.-L., Hayashi T., Shiga N., Yasukawa H., Schaper W., McKenna W.,
RA Yokoyama M., Schork N.J., Omens J.H., McCulloch A.D., Kimura A.,
RA Gregorio C.C., Poller W., Schaper J., Schultzeiss H.P., Chien K.R.;
RT "The cardiac mechanical stretch sensor machinery involves a Z disc
RT complex that is defective in a subset of human dilated
RT cardiomyopathy.";
RL Cell 111:943-955(2002).
CC -!- FUNCTION: Positive regulator of myogenesis. Could play a role in
CC mechanical stretch sensing.
CC -!- SUBCELLULAR LOCATION: Nuclear, associates with the actin
CC cytoskeleton (Potential).
CC -!- TISSUE SPECIFICITY: Cardiac and slow-twitch skeletal muscles.
CC -!- DISEASE: Defects in CSR3 are the cause of dilated cardiomyopathy
CC LM (CMDIM) [MIM:607482], a disorder characterized by cardiac
CC dilation and reduced systolic function.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U20324; AAA91104.1; -;
DR EMBL; U49837; AAA92571.1; -;
DR EMBL; U72898; AAD00189.1; -;
DR EMBL; U72894; AAD00189.1; -;
DR EMBL; U72895; AAD00189.1; JOINED.
DR EMBL; U72896; AAD00189.1; JOINED.
DR EMBL; U72897; AAD00189.1; JOINED.
DR EMBL; U72899; AAD00183.1; -;
DR EMBL; AF121260; AAF28868.1; -;
DR EMBL; BC005900; AAH05900.1; -;
DR EMBL; BC024010; AAH24010.1; -;
DR EMBL; BC057221; AAH57221.1; -;
DR HSSP; Q05158; IQLI.
DR Genew; HGNC:2472; CSR3.
DR MIM; 600824; -;
DR MIM; 607482; -;
DR GO; GO:0007519; P:myogenesis; TAS.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS50023; LIM_DOMAIN_2; 2.
KW Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis;
KW Disease mutation.
FT DOMAIN 10 61 LIM 1.
FT DOMAIN 63 78 GLY-RICH.
FT DOMAIN 64 69 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 120 171 LIM 2.
FT DOMAIN 177 185 GLY-RICH.
FT VARIANT 4 4 W -> R (in CMDIM).

FT FT CONFLICT 26 26 /FTID=VAR 015401.
FT SEQUENCE 194 AA; 20969 MW; FDB6E4F8D258C35F CRC64;
SQ
Query Match 34.5%; Score 48; DB 1; Length 194;
Best Local Similarity 34.6%; Pred. No. 4.4;
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;
QY 2 RPW----TNCSLDGRSVLKTGTTEKD 23
Db 138 KPWHKTCFRCACGKSLESTNVTDKD 163
RESULT 16
CSR3_MOUSE
ID_CSR3_MOUSE STANDARD; PRT; 194 AA.
AC P50462;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE LIM domain protein, cardiac (Muscle LIM protein) (Cysteine-rich
DE protein 3) (CRP3).
GN CSRP3 OR CLP OR MLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MF1; TISSUE=Mandible;
RX MEDLINE=96369959; PubMed=8773898;
RA Harrod G.V., Kettunen P.J., Jowett A.K.;
RT "Murine MLP: cloning and expression in the embryonic head."
RL J. Craniofac. Genet. Dev. Biol. 16:65-73(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX Hashimoto N., Ogashiwa M.;
RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Positive regulator of myogenesis.
CC -!- SUBCELLULAR LOCATION: Nuclear, associates with the actin
CC cytoskeleton (Potential).
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z49883; CAA90039.1; --
CC EMBL; D88791; EAA13721.1; --
CC EMBL; BC061131; AAH61131.1; --
CC PIR; S57472; S57472.
CC HSSP; Q05158; 1QLI.
CC MGD; MGI:1330824; Csrp3.
CC InterPro; IPR001781; LIM.
CC Pfam; PF00412; LIM; 2.
CC ProDom; PD000094; LIM; 2.
CC SMART; SM00132; LIM; 2.
CC PROSITE; PS00478; LIM DOMAIN 1; 2.
CC PROSITE; PS50023; LIM_DOMAIN_2; 2.
KW Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis.
FT DOMAIN 10 61 LIM 1.
FT DOMAIN 63 78 GLY-RICH.
FT DOMAIN 64 69 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 120 171 LIM 2.
FT DOMAIN 177 185 GLY-RICH.
SQ SEQUENCE 194 AA; 20895 MW; E35CF30CA17CB227 CRC64;
Query Match 34.5%; Score 48; DB 1; Length 194;
Best Local Similarity 34.6%; Pred. No. 4.4;
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;
QY 2 RPW----TNCSLDGRSVLKTGTTEKD 23
Db 138 KPWHKTCFRCACGKSLESTNVTDKD 163
RESULT 17
CSR3_RAT
ID_CSR3_RAT STANDARD; PRT; 194 AA.
AC P50463;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE LIM domain protein, cardiac (Muscle LIM protein) (Cysteine-rich
DE protein 3) (CRP3).
GN CSRP3 OR CLP OR MLP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis; TISSUE=Skeletal muscle;
RX MEDLINE=95042720; PubMed=7954791;
RA Arber S., Halder G., Caroni P.;
RT "Muscle LIM protein, a novel essential regulator of myogenesis,
RT promotes myogenic differentiation."
RL Cell 79:221-231(1994).
CC -!- FUNCTION: Positive regulator of myogenesis.
CC -!- SUBCELLULAR LOCATION: Nuclear, associates with the actin
CC cytoskeleton.
CC -!- TISSUE SPECIFICITY: High in striated muscle and adult heart.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X81193; CAA57065.1; --
CC PIR; A55099; A55099.
CC HSSP; Q05158; 1QLI.
CC InterPro; IPR001781; LIM.
CC Pfam; PF00412; LIM; 2.
CC


```
Best Local Similarity 32.0%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 187 CQPHTRCEIQGLVEAAPGTSYSDTI 211

RESULT 21
RRPO_BBV STANDARD; PRT; 998 AA.
ID RRPO_BBV AC Q96631;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (RdRp) (RNA replicase)
DE (Protein A).
OS Black beetle virus (BBV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nodaviridae;
OC Alphaviruses.
OX NCBI_TaxID=12285;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85210903; PubMed=3839022;
RA Dasmahapatra B., Dasgupta R., Ghosh A., Kaesberg P.;
RT "Structure of the black beetle virus genome and its functional
implications.";
RL J. Mol. Biol. 182:183-189(1985).
RN [2]
RP PARTIAL PRELIMINARY SEQUENCE FROM N.A.
RX MEDLINE=85042104; PubMed=6495657;
RA Guarino L.A., Ghosh A., Dasmahapatra B., Dasgupta R., Kaesberg P.;
RT "Sequence of the black beetle virus subgenomic RNA and its location in
the viral genome.";
RL Virology 139:190-203(1984).
CC -!- FUNCTION: Replicates the viral genome which is composed of two RNA
segments, RNA1 and RNA2.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
{RNA}(N).
CC -!- SIMILARITY: Belongs to the nodaviruses RNA polymerase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X02396; CAA26238.1; -
DR EMBL; K02560; AAA42742.1; ALT_FRAME.
DR PIR; S78471; QQBBI.
DR InterPro; IPR007095; RNA_pol_DS_PS.
KW Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 998 AA; 112196 MW; A57DA34AFE0A296B CRC64;

Query Match 33.8%; Score 47; DB 1; Length 998;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7
Db 262 CRPWTDC 268

RESULT 22
RRPO_BOOLV STANDARD; PRT; 998 AA.
ID RRPO_BOOLV AC Q92J0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (RdRp) (RNA replicase)
DE (Protein A).
OS Flock house virus (FHV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nodaviridae;
OC Alphaviruses.
OX NCBI_TaxID=12287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21351039; PubMed=11457991;
RA Johnson K.N., Johnson K.L., Dasgupta R., Gratsch T., Ball L.A.;
RT "Comparisons among the larger genome segments of six nodaviruses and
their encoded RNA replicases.";
RL J. Gen. Virol. 82:1855-1866(2001).
CC -!- FUNCTION: Replicates the viral genome which is composed of two RNA
segments, RNA1 and RNA2.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
{RNA}(N).
CC -!- SIMILARITY: Belongs to the nodaviruses RNA polymerase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF329080; AAK15751.1; -
DR InterPro; IPR007095; RNA_pol_DS_PS.
KW Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 998 AA; 111203 MW; 7FAFFB4FC7329253 CRC64;

Query Match 33.8%; Score 47; DB 1; Length 998;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7
Db 262 CRPWTDC 268

RESULT 23
RRPO_FHV STANDARD; PRT; 998 AA.
ID RRPO_FHV AC Q66929;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (RdRp) (RNA replicase)
DE (Protein A).
OS Flock house virus (FHV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nodaviridae;
OC Alphaviruses.
OX NCBI_TaxID=12287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21351039; PubMed=11457991;
RA Johnson K.N., Johnson K.L., Dasgupta R., Gratsch T., Ball L.A.;
RT "Comparisons among the larger genome segments of six nodaviruses and
their encoded RNA replicases.";
RL J. Gen. Virol. 82:1855-1866(2001).
CC -!- FUNCTION: Replicates the viral genome which is composed of two RNA
segments, RNA1 and RNA2.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
{RNA}(N).
CC -!- SIMILARITY: Belongs to the nodaviruses RNA polymerase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF329080; AAK15751.1; -
DR InterPro; IPR007095; RNA_pol_DS_PS.
KW Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 998 AA; 111203 MW; 7FAFFB4FC7329253 CRC64;
```

```
DR EMBL; X77156; CAA54399.1; -.
DR PIR; S41397; S41397.
DR InterPro; IPR007095; RNA_pol_DS_Ps.
KW Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 998 AA; 112187 MW; E9A64CE06555B21C CRC64;

Query Match      33.8%; Score 47; DB 1; Length 998;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPWTNC 7
Db      262 CRPWTDC 268

RESULT 24
TR18_HUMAN STANDARD; PRT; 241 AA.
ID Q9Y5U5; O95851; Q9NYJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor).
DE TNFRSF18 OR GTR OR AITR.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2 AND
RP TRAF3.
RC TISSUE=Bone marrow;
RX MEDLINE=99175482; PubMed=10074428;
RA Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
RA Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA Ashkenazi A.;
RA "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR.";
RL Curr. Biol. 9:215-218(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=T-cell;
RX MEDLINE=99156876; PubMed=10037686;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA Liu D., Wang S.-X., Kwon B.S.;
RA "Identification of a novel activation-inducible protein of the tumor
RT necrosis factor receptor superfamily and its ligand.";
RL J. Biol. Chem. 274:6056-6061(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 7:408-410(2000).
CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y5U5-1; Sequence=Displayed;
CC Name=2; Synonyms=GTR-D;
CC IsoId=Q9Y5U5-2; Sequence=VSP_006508;
```

```
CC -!- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC leukocytes and weakly in spleen.
CC -!- INDUCTION: Upregulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF125304; AAD22635.1; -.
CC EMBL; AF117297; AAD19694.1; -.
CC EMBL; AF241229; AAF63506.1; -.
CC Genew; HGNC:11914; TNFRSF18.
CC MIM; 603905; -.
CC GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR001368; TNFR_c6.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
CC PROSITE; PS00050; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 241
FT -----
FT DOMAIN 26 162
FT TRANSMEM 163 183
FT DOMAIN 184 241
FT REPEAT 34 72
FT REPEAT 74 112
FT REPEAT 115 153
FT DISULFID 34 49
FT DISULFID 74 86
FT DISULFID 81 94
FT DISULFID 115 134
FT DISULFID 128 153
FT CARBOHYD 146 146
FT VARSPLIC 135 241
FT -----
FT POTENTIAL.
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 18.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TQFGLTVFPNGKTHNAVCPSPPAEPLGWLTVVLLAVAA
FT CVLLLTSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDAR
FT SCQFPEEERGESAEKGRGLDW -> CWCRRRPKTPPE
FT AASSPRKSGASDRQRRRGWETCGCEPGRPPGPTAASPSP
FT GAPQAAGALRSALGRALLFPWQKWVQEGGSDQRPGPCSSAA
FT AAGPCRRERETQSWPPSSLAGPDGVGS (in isoform
FT 2).
FT /FTid=VSP_006508.
FT SQCMWPRE -> K (IN REF. 2).
FT 90DC3B4AA7E82CBE CRC64;
FT CONFLICT 194 201
FT SEQUENCE 241 AA; 26000 MW;
FT -----
Query Match      33.1%; Score 46; DB 1; Length 241;
Best Local Similarity 54.5%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDG 11
Db      128 CKPWTDC TQFG 138
|:|:|:|:|:|:|
|:|:|:|:|:|:|

RESULT 25
CGH2_HSVSA
ID CGH2_HSVSA STANDARD; PRT; 254 AA.
AC Q01043;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclin homolog (V-cyclin).
GN 72 OR ECLF2.
OS Herpesvirus saimiri (strain 11).
```

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gamaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10383;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92333688; PubMed=1321287;

RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,

RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,

RA Honess R.W.;

RT "Primary structure of the herpesvirus saimiri genome.";

RL J. Virol. 66:5047-5058(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92230228; PubMed=1314457;

RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;

RT "Analysis of nucleotide sequence of the rightmost 43 kbp of

RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic

RT organization between HVS and Epstein-Barr virus.";

RL Virology 188:296-310(1992).

RN [3]

RP SIMILARITY TO G-PROTEIN COUPLED RECEPTORS.

RX MEDLINE=92115001; PubMed=1309943;

RA Nicholas J., Cameron K.R., Honess R.W.;

RT "Herpesvirus saimiri encodes homologues of G protein-coupled

RT receptors and cyclins.";

RL Nature 355:362-365(1992).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (3.00 ANGSTROMS) OF 22-250.

RX MEDLINE=99197290; PubMed=10368294;

RA Schulze-Gahmen U., Jung J.U., Kim S.-H.;

RT "Crystal structure of a viral cyclin, a positive regulator of cyclin-

RT dependent kinase 6.";

RL Structure 7:245-254(1999).

CC -!- FUNCTION: MAY BE HIGHLY RELEVANT TO THE PROCESS OF CELLULAR

CC TRANSFORMATION AND RAPID T-CELL PROLIFERATION EFFECTED BY HVS

CC DURING LATENT INFECTIONS OF T-CELLS IN SUSCEPTIBLE HOSTS.

CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; S76368; AAB21115.1; -.

DR EMBL; X64346; CAA45695.1; -.

DR EMBL; M86409; AAA46148.1; -.

DR PDB; 1BU2; 15-JUN-99.

DR PDB; 1JOW; 27-FEB-02.

DR InterPro; IPR006670; Cyclin.

DR InterPro; IPR006671; Cyclin_N.

DR Pfam; PF00134; cyclin; 1.

DR SMART; SM00385; CYCLIN; 1.

DR PROSITE; PS00292; CYCLINS; 1.

KW Cyclin; Cell cycle; Cell division; 3D-structure.

FT HELIX 24 29

FT TURN 30 32

FT TURN 40 43

FT HELIX 49 65

FT TURN 66 67

FT TURN 70 71

FT HELIX 72 83

FT TURN 84 86

FT TURN 91 93

FT HELIX 94 108

FT HELIX 116 121

FT TURN 122 125

FT HELIX 129 142

FT TURN 143 145

FT HELIX 152 155

FT HELIX 156 162

FT TURN 163 164

FT TURN 167 168

FT HELIX 170 184

FT TURN 185 186

FT TURN 188 189

FT HELIX 190 192

FT HELIX 195 209

FT TURN 210 210

FT TURN 216 216

FT HELIX 217 220

FT HELIX 221 223

FT TURN 224 226

FT HELIX 230 242

FT TURN 243 244

FT HELIX 247 249

SQ SEQUENCE 254 AA; 28637 MW; B682EB10111207F4 CRC64;

Query Match 33.1%; Score 46; DB 1; Length 254;

Best Local Similarity 44.8%; Pred. No. 12;

Matches 13; Conservative 1; Mismatches 11; Indels 4; Gaps 1;

OY 1 CRPWTNCSLDGRSVLKTGT-----TEKDVV 25

||||| :|:|:|

Db 214 CRPWTCTYLELSSILNFSNTVTVTVDQV 242

RESULT 26

ASG2_ECOLI

ID ASG2_ECOLI STANDARD; PRT; 348 AA.

AC P00805;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE L-asparaginase II precursor (BC 3.5.1.1) (L-asparagine

DE amidohydrolase II) (L-ASNase II) (Colaspase).

GN ANSB OR B2957.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90170867; PubMed=2407723;

RA Jennings M.P., Beacham I.R.;

RT "Analysis of the Escherichia coli gene encoding L-asparaginase II,

RT anSB, and its regulation by cyclic AMP receptor and FNR proteins.";

RL J. Bacteriol. 172:1491-1498(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=90382683; PubMed=2144836;

RA Bonthron D.T.;

RT "L-asparaginase II of Escherichia coli K-12: cloning, mapping and

RT sequencing of the anSB gene.";

RL Gene 91:101-105(1990).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [4]

RP SEQUENCE OF 23-348.

RX MEDLINE=80135739; PubMed=6766894;

RA Maita T., Matsuda G.;

RT "The primary structure of L-asparaginase from Escherichia coli.";

RL Hoppe-Seyler's Z. Physiol. Chem. 361:105-117(1980).

RN [5]

RP PARTIAL SEQUENCE.

RX MEDLINE=80048329; PubMed=387570;
RA Maiba T., Morokuma K., Matsuda G.;
RT "Amino acid sequences of the tryptic peptides from carboxymethylated
RT L-asparaginase from *Escherichia coli*.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:1483-1495(1979).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=77140944; PubMed=321449;
RA Peterson R.G., Richards F.F., Handschumacher R.E.;
RT "Structure of peptide from active site region of *Escherichia coli* L-
RT asparaginase.";
RL J. Biol. Chem. 252:2072-2076(1977).
RN [7]
RP SUBUNITS.
RX MEDLINE=73007901; PubMed=4561256;
RA Greenquist A.C., Wriston J.C. Jr.;
RT "Chemical evidence for identical subunits in L-asparaginase from
RT *Escherichia coli* B.";
RL Arch. Biochem. Biophys. 152:280-286(1972).
RN [8]
RP ACTIVE SITE THR-34.
RX MEDLINE=91293312; PubMed=1906013;
RA Harms E., Wehner A., Aung H.P., Roehm K.H.;
RT "A catalytic role for threonine-12 of *E. coli* asparaginase II as
RT established by site-directed mutagenesis.";
RL FEBS Lett. 285:55-58(1991).
RN [9]
RP MUTAGENESIS OF HISTIDINE RESIDUES.
RX MEDLINE=92394146; PubMed=1521538;
RA Wehner A., Harms E., Jennings M.P., Beacham I.R., Derst C., Bast P.,
RA Roehm K.H.;
RT "Site-specific mutagenesis of *Escherichia coli* asparaginase II. None
RT of the three histidine residues is required for catalysis.";
RL Eur. J. Biochem. 208:475-480(1992).
RN [10]
RP MUTAGENESIS OF THREONINE AND SERINE RESIDUES.
RX MEDLINE=93165634; PubMed=1287659;
RA Ders C., Henseling J., Roehm K.H.;
RT "Probing the role of threonine and serine residues of *E. coli*
RT asparaginase II by site-specific mutagenesis.";
RL Protein Eng. 5:785-789(1992).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=93165718; PubMed=8434007;
RA Swain A.L., Jaskolski M., Housset D., Rao J.K.M., Wlodawer A.;
RT "Crystal structure of *Escherichia coli* L-asparaginase, an enzyme used
RT in cancer therapy.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1474-1478(1993).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT VAL-111.
RX MEDLINE=96305806; PubMed=8706862;
RA Palm G.J., Lubkowski J., Derst C., Schleper S., Roehm K.H.,
RA Wlodawer A.;
RT "A covalently bound catalytic intermediate in *Escherichia coli*
RT asparaginase: crystal structure of a Thr-89-Val mutant.";
RL FEBS Lett. 390:211-216(1996).
CC -!- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).
CC -!- SUBUNIT: Homotetramer.
CC -!- INDUCTION: BY CAMP AND ANAEROBIOSIS.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- PHARMACEUTICAL: Available under the names Crastinin (Bayer),
CC Elspar (Merck), Kidrolase (Rhône-Poulenc) and Leunase (Kyowa).
CC Also available as a PEG-conjugated form (pegaspargase) under the
CC name Oncaspar (Enzon). Used as an antineoplastic in chemotherapy.
CC Reduces the quantity of asparagine available to cancer cells.
CC -!- MISCELLANEOUS: KM = 1.15 X 10⁻⁵ M.
CC -!- MISCELLANEOUS: *E. coli* CONTAINS TWO L-ASPARAGINASE ISOENZYMES:
CC L-ASPARAGINASE I, A LOW-AFFINITY ENZYME LOCATED IN THE CYTOPLASM,
CC AND L-ASPARAGINASE II, A HIGH-AFFINITY SECRETED ENZYME.
CC -!- SIMILARITY: Belongs to the asparaginase 1 family.
CC -!- DATABASE: NAME=Worthington enzyme manual;
CC WWW="http://www.worthington-biochem.com/ASPR/".
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34277; AAA24062.1; -.
DR EMBL; M34234; AAA23445.1; -.
DR EMBL; U28377; AAA69124.1; -.
DR EMBL; AE000378; AAC75994.1; -.
DR PIR; A35132; XDEC.
DR PDB; 3ECA; 31-OCT-93.
DR PDB; 4ECA; 16-JUN-97.
DR PDB; 1HO3; 07-MAR-01.
DR EcoGene; EG10046; ansB.
DR InterPro; IPR004550; AsnASE II.
DR InterPro; IPR006034; Asp/Glutamase.
DR Pfam; PF00710; Asparaginase; 1.
DR PRINTS; PR00139; ASNGLNASE.
DR ProDom; PD003221; Asp/Glutamase; 1.
DR TIGRFAMs; TIGR00520; asnASE II; 1.
DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
KW Hydrolase; Signal; Periplasmic; Pharmaceutical; 3D-structure;
KW Complete proteome.
FT SIGNAL 1 22
FT CHAIN 23 348 L-ASPARAGINASE II.
FT ACT_SITE 34 34
FT ACT_SITE 111 111 BY SIMILARITY.
FT ACT_SITE 112 112 BY SIMILARITY.
FT ACT_SITE 184 184 BY SIMILARITY.
FT DISULFID 99 127
FT BINDING 141 141 INVOLVED IN SUBSTRATE BINDING.
FT MUTAGEN 34 34 T->A: ALMOST NO ACTIVITY.
FT CONFLICT 49 49 V -> A (IN REF. 4).
FT CONFLICT 86 86 N -> D (IN REF. 4).
FT CONFLICT 132 132 MISSING (IN REF. 4).
FT CONFLICT 156 156 MISSING (IN REF. 4).
FT CONFLICT 171 171 MISSING (IN REF. 4).
FT CONFLICT 206 206 N -> D (IN REF. 4).
FT CONFLICT 268 268 N -> D (IN REF. 4).
FT CONFLICT 274 274 S -> T (IN REF. 4).
FT CONFLICT 285 285 T -> D (IN REF. 4).
FT CONFLICT 290 290 MISSING (IN REF. 4).
FT CONFLICT 330 330 MISSING (IN REF. 4).
FT STRAND 25 32
FT TURN 34 36
FT STRAND 38 38
FT STRAND 48 48
FT HELIX 54 59
FT TURN 60 60
FT TURN 62 63
FT HELIX 64 66
FT TURN 67 67
FT STRAND 69 78
FT HELIX 80 82
FT HELIX 85 99
FT TURN 100 101
FT STRAND 104 108
FT TURN 112 113
FT HELIX 114 124
FT STRAND 131 134
FT TURN 140 141
FT TURN 143 144
FT HELIX 147 159
FT HELIX 161 163
FT TURN 164 165
FT STRAND 169 172
FT TURN 173 174
FT STRAND 175 178
FT TURN 179 181


```
FT STRAND 182 184
FT STRAND 186 186
FT TURN 190 191
FT STRAND 193 195
FT TURN 196 198
FT STRAND 202 205
FT TURN 206 207
FT STRAND 208 211
FT HELIX 220 222

Query Match 33.1%; Score 46; DB 1; Length 348;
Best Local Similarity 69.2%; Pred. No. 17;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTT 21
    |||||
Db 177 LDGRDVTNTTID 189

RESULT 27
KHSE_CORGL STANDARD; PRT; 308 AA.
AC P07128; P08210;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homoserine kinase (EC 2.7.1.39) (HK).
GN THRB OR CGL1184.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=88216182; PubMed=2835591;
RA Peoples O.P., Liebi W., Bodis M., Maeng P.J., Follettie M.T.,
RA Archer J.A.C., Sinskey A.J.;
RT "Nucleotide sequence and fine structural analysis of the
RT Corynebacterium glutamicum hom-thrB operon.";
RL Mol. Microbiol. 2:63-72(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13869;
RX MEDLINE=87231082; PubMed=3035505;
RA Mateos L.M., del Real G., Aguilar A., Martin J.F.;
RT "Nucleotide sequence of the homoserine kinase (thr B) gene of
RT Brevibacterium lactofermentum.";
RL Nucleic Acids Res. 15:3922-3922(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + L-homoserine = ADP + O-phospho-L-
CC homoserine.
CC -!- PATHWAY: Threonine biosynthesis from aspartate; fourth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the GMP kinase family. Homoserine kinase
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; Y00546; CAA68615.1; -
CC EMBL; Y00140; CAA68332.1; -
CC EMBL; AP005277; BAB98577.1; -
DR
```

```
DR PIR; S00866; KIFKMG.
DR HAMAP; MF_00384; -; 1.
DR InterPro; IPR006204; GHMP_kinase.
DR InterPro; IPR006203; GHMPkinse_ATP.
DR InterPro; IPR000870; Homoser_Kin.
DR Pfam; PF00288; GHMP_kinases; 1.
DR PRINTS; PR00958; HOMSERKINASE.
DR TIGREAFs; TIGR00191; thrB; 1.
DR PROSITE; PS00627; GHMP_KINASES_ATP; 1.
KW Threonine biosynthesis; Transferase; Kinase; ATP-binding;
KW Complete proteome.
FT INIT MET 0 0
FT NP_BIND 94 104 ATP (POTENTIAL).
FT CONFLICT 245 245 I -> V (IN REF. 2).
SQ SEQUENCE 308 AA; 32489 MW; 492AF7975C012623 CRC64;

Query Match 32.4%; Score 45; DB 1; Length 308;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WTNCSLDGRS 13
    |||
Db 152 WTNLSIDGKS 161

RESULT 28
T11B_HUMAN
ID T11B_HUMAN STANDARD; PRT; 401 AA.
AC O00300; O60236; Q9UHP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
```



```

receptor for TRAIL and protect against apoptosis. TRAIL binding
blocks the inhibition of osteoclastogenesis.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
lymph node, trachea, adrenal gland, testis, and bone marrow.
Detected at very low levels in brain, placenta and skeletal
muscle. Highly expressed in fetal kidney, liver and lung.
-!- INDUCTION: Upregulated by increasing calcium-concentration in the
medium and estrogens. Downregulated by glucocorticoids.
-!- PTM: N-glycosylated. Contains sialic acid residues.
-!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
-!- SIMILARITY: Contains 2 death domains.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; U94332; AAB53709.1; -.
EMBL; AB002146; BAA25910.1; -.
EMBL; AB008822; BAA32076.1; -.
EMBL; AB008821; BAA32076.1; JOINED.
EMBL; BC030155; AAH30155.1; -.
EMBL; AF134187; AAF20168.1; -.
HSP; P25942; ICDF.
Genew; HGNC:11909; TNFRSF11B.
MIM; 602643; -.
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0005125; F:cytokine activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR00488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS0017; DEATH DOMAIN; FALSE_NEG.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS00050; TNFR_NGFR_2; 2.
Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
SIGNAL 1 21
CHAIN 22 401
TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 11B.
REPEAT 24 62
TNFR-CYS 1.
REPEAT 65 105
TNFR-CYS 2.
REPEAT 107 142
TNFR-CYS 3.
REPEAT 145 185
TNFR-CYS 4.
DOMAIN 198 269
DEATH 1.
DOMAIN 270 365
DEATH 2.
SITE 400 400
INVOLVED IN DIMERIZATION.
DISULFID 41 54
BY SIMILARITY.
DISULFID 44 62
BY SIMILARITY.
DISULFID 65 80
BY SIMILARITY.
DISULFID 83 97
BY SIMILARITY.
DISULFID 87 105
BY SIMILARITY.
DISULFID 107 118
BY SIMILARITY.
DISULFID 124 142
BY SIMILARITY.
DISULFID 145 160
BY SIMILARITY.
DISULFID 166 185
BY SIMILARITY.
CARBOHYD 98 98
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 152 152
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 165 165
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 178 178
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 289 289
N-LINKED (GLCNAC. .) (POTENTIAL).
VARIANT 3 3
X -> N.
/FTId=VAR_013439.

```

TISSUE=Eye;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loeuquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
SEQUENCE OF 22-36 AND 378-401.
MEDLINE=98238645; PubMed=9571159;
Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H., Morinaga T., Tsuda E., Higashio K.;
"Characterization of monomeric and homodimeric forms of osteoclastogenesis inhibitory factor";
Biochem. Biophys. Res. Commun. 245:382-387(1998).
[6]
SEQUENCE OF 22-393 FROM N.A.
TISSUE=Placenta;
He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Cloning and expression of osteoprotegerin from Homo sapiens."; Acta Biochim. Biophys. Sin. 31:680-684(1999).
[7]
SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
MEDLINE=97312536; PubMed=9168977;
Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F., Morinaga T., Higashio K.;
"Isolation of a novel cytokine from human fibroblasts that specifically inhibits osteoclastogenesis."; Biochem. Biophys. Res. Commun. 234:137-142(1997).
[8]
TRAIL BINDING.
MEDLINE=98269100; PubMed=9603945;
Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C., Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A., James I.E., Rosenberg M., Lee J.C., Young P.R.;
"Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL."; J. Biol. Chem. 273:14363-14367(1998).
[9]
CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
MEDLINE=98148059; PubMed=9478964;
Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E., Morinaga T., Higashio K.;
"Characterization of structural domains of human osteoclastogenesis inhibitory factor."; J. Biol. Chem. 273:5117-5123(1998).
[10]
REVIEW.
MEDLINE=21395914; PubMed=11505389;
Hofbauer L.C., Neubauer A., Heufelder A.E.;
"Receptor activator of nuclear factor-kappaB ligand and osteoprotegerin: potential implications for the pathogenesis and treatment of malignant bone diseases."; Cancer 92:460-470(2001).
-!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy

FT MUTAGEN 400 400 C->S: ABOLISHES DIMERIZATION.
FT MUTAGEN 400 401 MISSING: ABOLISHES DIMERIZATION.
FT CONFLICT 263 263 D.-> A (IN REF. 1).
SQ SEQUENCE 401 AA; 46040 MW; EDF448B67D86C71E CRC64;

Query Match 32.4%; Score 45; DB 1; Length 401;
Best Local Similarity 39.1%; Pred. No. 28;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTEKD 23
||| | : : |
Db 160 CRKHTNCSVFGLLITQKGNATHD 182

RESULT 29

T11B_RAT STANDARD; PRT; 401 AA.

AC O08727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
(Osteoprotegerin).
GN TNFRSF11B OR OPB.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

SEQUENCE FROM N.A.

TISSUE=Embryonic intestine;

RX MEDLINE=97262071; PubMed=9108485;

RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
RL Cell 89:309-319(1997).

CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
its function in osteoclastogenesis. Inhibits the activation of
osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
seems to depend on the local RANKL/OPG ratio. May also play a role
in preventing arterial calcification. May act as decoy receptor
for TRAIL and protect against apoptosis. TRAIL binding blocks the
inhibition of osteoclastogenesis (By similarity).

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- INDUCTION: Upregulated by osteopontin.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 2 death domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U94330; AAB53707.1; -.

DR HSSP; P25942; ICDF.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00017; DEATH DOMAIN; FALSE_NEG.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00050; TNFR_NGFR_2; 2.

DR Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 11B.
FT REPEAT 24 62 TNFR-CYS 1.
FT REPEAT 65 105 TNFR-CYS 2.
FT REPEAT 107 142 TNFR-CYS 3.
FT REPEAT 145 185 TNFR-CYS 4.
FT DOMAIN 198 269 DEATH 1.
FT DOMAIN 270 365 DEATH 2.
FT SITE 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT DISULFID 166 185 BY SIMILARITY.
FT CARBOHYD 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 401 AA; 46192 MW; FEC6A31FID4E573A CRC64;

Query Match 32.4%; Score 45; DB 1; Length 401;
Best Local Similarity 40.0%; Pred. No. 28;
Matches 10; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTEKD 25
||| | : : |
Db 160 CRKHTNCSVFGLLITQKGNATHDNV 184

RESULT 30

RBA1_CAEEL

ID RBA1_CAEEL STANDARD; PRT; 412 AA.
AC P90917;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Tfp-Asp repeats containing protein RBA-1.

GN RBA-1 OR K07A1.11.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Percy C.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 6 WD repeats.

CC -!- SIMILARITY: Belongs to the WD-repeat RBA46/RBAP48/MS11 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z81097; CAB03172.1; -.

DR PIR; T23385; T23385.

DR WormPep; K07A1.11; CE11860.

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 5.

DR PRINTS; PR00320; GPROTEINRPT.

DR SMART; SM00320; WD40; 5.

DR PROSITE; PS00678; WD_REPEATS_1; 2.

DR PROSITE; PS00082; WD_REPEATS_2; 4.

DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

KW Repeat; WD repeat. 117 157 WD 1.
FT REPEAT 117 157 WD 1.
FT REPEAT 169 209 WD 2.
FT REPEAT 219 259 WD 3.
FT REPEAT 262 302 WD 4.
FT REPEAT 306 346 WD 5.
FT REPEAT 365 405 WD 6.
SQ SEQUENCE 412 AA; 46691 MW; 7F65FA7F4F2D7772 CRC64;

Query Match 32.4%; Score 45; DB 1; Length 412;
Best Local Similarity 37.5%; Pred. No. 29;
Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 2 RPWTNCSLDGRSVLKTGTTEKDVV 25
Db 379 RPWTICSDEFNALQVWEVNSLV 402

RESULT 31
TR21 MOUSE STANDARD; PRT; 655 AA.
AC Q9EP05; Q91W77; Q91XH9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F., Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6 (DR6).";
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT "Murine DR6: murine TNFR-related death receptor-6.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP FUNCTION.
RX MEDLINE=21571606; PubMed=11714751;

RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal kinase activity and T cell differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448 (2001).
CC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By similarity). May activate JNK and be involved in T-cell differentiation.
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis. May be involved in T-cell differentiation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen, thymus, testis, prostate, ovary, small intestine, colon, brain, lung and kidney, and in fetal brain, liver and lung. Detected at lower levels in adult peripheral blood leukocytes, lung, and in fetal muscle, heart, kidney, small intestine and skin. Detected in T-cells, B-cells and monocytes. In T-cells expression is highest in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF322069; AAG38115.1; -.
CC EMBL; AY043489; AAK74193.1; -.
CC EMBL; BC016420; AAH16420.1; -.
CC HSP; O14763; 1D0G.
CC MGD; MGI:2151075; Tnftrsf21.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00531; death; 1.
CC Pfam; PF00020; TNFR_C6; 4.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS0017; DEATH DOMAIN; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS0050; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 21.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT DEATH.
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT TNFR-CYS 4.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT W -> L (IN REF. 1).
FT M -> I (IN REF. 3).
FT CONFLICT 352 353
FT SEQUENCE 655 AA; 71982 MW; 5EC7C51C7C99EFF7 CRC64;
SQ

DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 357 WNT-9B PROTEIN.
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 357 AA; 38970 MW; E1221629A0294CB6 CRC64;

Query Match 31.7%; Score 44; DB 1; Length 357;
 Best Local Similarity 57.9%; Pred. No. 36;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 2;

QY 4 WTNCSLDGRS-VLKTGTTE 21
 Db 98 W-NCSLEGRGTGLLKRGPK 115

RESULT 34
 LEU3_BUCUE STANDARD; PRT; 364 AA.
 AC Q9EVH5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)
 DE (IMDH) (3-IPM-DH).
 GN LEUB.
 OS Buchnera aphidicola (subsp. Uroleucon erigeronensis).
 OG Plasmid pLeu (pBAP1).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=168385;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20576185; PubMed=11133977;
 RA Wernegreen J.J., Moran N.A.;
 RT "Vertical transmission of biosynthetic plasmids in aphid endosymbionts
 (Buchnera).";
 RL J. Bacteriol. 183:785-790(2001).
 CC -!- FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-
 methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-
 oxopentanoate. The product decarboxylates to 4-methyl-2-
 oxopentanoate.
 CC -!- CATALYTIC ACTIVITY: 3-carboxy-2-hydroxy-4-methylpentanoate +
 NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.
 CC -!- PATHWAY: Leucine biosynthesis; third step.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the isocitrate and isopropylmalate
 dehydrogenases family. Leub subfamily 1.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; AF197452; AAC31390.1; -.
 DR HSSP; P37412; 1CNZ.
 DR HAMAP; MF_01033; -; 1.
 DR InterPro; IPR001804; Isodh.
 DR InterPro; IPR004429; LeuB.
 DR Pfam; PF00180; isodh; 1.
 DR TIGRFAMs; TIGR00169; leuB; 1.
 DR PROSITE; PS00470; IDH_IMDH; 1.
 KW Oxidoreductase; Leucine biosynthesis; NAD; Plasmid.
 SQ SEQUENCE 364 AA; 40542 MW; 0B94A8A092CB7FCD CRC64;

Query Match 31.7%; Score 44; DB 1; Length 364;
 Best Local Similarity 47.4%; Pred. No. 36;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 CSLDGRSVLKTGTTEKDVV 25
 Db 191 CSLDKSNVLKSSILWKEIV 209

RESULT 35
 SCAG_XENLA STANDARD; PRT; 660 AA.
 ID SCAG_XENLA
 AC P51171;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amiloride-sensitive sodium channel gamma-subunit (Epithelial Na+
 channel gamma subunit) (Gamma ENaC) (Nonvoltage-gated sodium channel 1
 gamma subunit) (SCNEG) (Gamma NaCH).
 DE Xenopus laevis (African clawed frog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=95358264; PubMed=7631745;
 RA Puoti A., May A., Canessa C.M., Horisberger J.-D., Schild L.,
 Rossier B.C.;
 RA "The highly selective low-conductance epithelial Na channel of
 Xenopus laevis A6 kidney cells.";
 RT Am. J. Physiol. 269:C188-C197(1995).
 CC -!- FUNCTION: Sodium permeable non-voltage-sensitive ion channel
 inhibited by the diuretic amiloride. Mediates the electrodiffusion
 of the luminal sodium (and water, which follows osmotically)
 through the apical membrane of epithelial cells. Controls the
 reabsorption of sodium in kidney, colon, lung and sweat glands.
 CC Also plays a role in taste perception.
 CC -!- SUBUNIT: Heterotetramer of two alpha, one beta and one gamma
 subunit. A delta subunit can replace the alpha subunit (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: Phosphorylated on serine and threonine residues (By
 similarity).
 CC -!- PTM: Ubiquitinated; this targets individual subunits for
 proteasome-mediated degradation (By similarity).
 CC -!- SIMILARITY: Belongs to the amiloride-sensitive sodium channel
 family.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; U25342; AAA74972.1; -.
 DR PIR; I51684; I51684.
 DR InterPro; IPR004724; EnaC.
 DR InterPro; IPR001873; Na+channel_ASC.
 DR Pfam; PF00858; ASC; 1.
 DR PRINTS; PR01078; AMINACHANNEL.
 DR TIGRFAMs; TIGR00859; ENaC; 1.
 DR PROSITE; PS01206; ASC; 1.
 KW Ion transport; Sodium transport; Ionic channel; Transmembrane;
 KW Glycoprotein; Phosphorylation; Ubl conjugation; Sodium channel.
 FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 56 76 POTENTIAL.
 FT DOMAIN 77 545 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 546 566 POTENTIAL.
 FT DOMAIN 567 660 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).


```

RX MEDLINE=98344831; PubMed=9681506;
RA Tseng C.-P., Ely B.D., Li Y., Pong R.-C., Hsieh J.-T.;
RT "Regulation of rat DOC-2 gene during castration-induced rat ventral
RT prostate degeneration and its growth inhibitory function in human
RT prostatic carcinoma cells.";
RL Endocrinology 139:3542-3553(1998).
RN [2]
RP SEQUENCE OF 2-47; 117-189; 634-687 AND 753-768 FROM N.A.
RC TISSUE=Kidney, and Prostate;
RA Lau K.M., Mok S.C., Ho S.M.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Component of the CSF-1 signal transduction pathway (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=p82;
CC IsoId=O88797-1; Sequence=Displayed;
CC Name=p59;
CC IsoId=O88797-2; Sequence=VSP_004184;
CC -!- TISSUE SPECIFICITY: Prostate.
CC -!- DOMAIN: The PID domain specifically binds to the Asn-Pro-Xaa-
CC Tyr(P) motif found in many tyrosine-phosphorylated proteins
CC including growth factor receptors.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Contains 1 PID domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U95177; AAC33405.1; -
DR EMBL; U95178; AAC33406.1; -
DR EMBL; AF045657; AAC03360.1; -
DR EMBL; AF045658; AAC03361.1; -
DR EMBL; AF045659; AAC03362.1; -
DR EMBL; AF045660; AAC03363.1; -
DR InterPro: IPR006020; PTB_PID.
DR Pfam: PF00640; PID; 1.
DR SMART: SM00462; PTB; 1.
DR PROSITE: PS01179; PID; 1.
KW Alternative splicing; Phosphorylation.
FT DOMAIN 45 196
FT VARSPLIC 230 447 Missing (in isoform p59).
FT CONFLICT 3 4 NE -> TN (IN REF. 2).
FT CONFLICT 186 186 N -> K (IN REF. 2).
FT CONFLICT 675 675 S -> P (IN REF. 2).
FT CONFLICT 764 768 GNPPA -> WKSFC (IN REF. 2).
SQ SEQUENCE 768 AA; 82376 MW; 930FB25248ADAC6E CRC64;

Query Match 31.7%; Score 44; DB 1; Length 768;
Best Local Similarity 41.7%; Pred. No. 83;
Matches 10; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 2 RPWTNCSLDGRSVL--KTGTTEKD 23
Db 92 RIWVNISLSGIKIIDEKTGVTEHE 115

RESULT 38
DAB2 HUMAN
ID DAB2 HUMAN STANDARD; PRT; 770 AA.
AC P98082; Q13598; Q9BTY0; Q9UK04;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Disabled homolog 2 (Differentially expressed protein 2) (DOC-2).
GN DAB2 OR DOC2.
OS Homo sapiens (Human).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96301397; PubMed=8660969;
RA Albertsen H.M., Smith S.A., Melis R., Williams B., Holik P.,
RA Stevens J., White R.;
RT "Sequence, genomic structure, and chromosomal assignment of human
RT DOC-2.";
RL Genomics 33:207-213(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Sheng Z., He J., Sun W., Smith E.R., Fazili Z., Feng D.B., Xu X.;
RT "Gene structure, sequence, and promoter of human disabled-2.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=99270207; PubMed=10340382;
RA Fazili Z., Sun W., Mittelstaedt S., Cohen C., Xu X.-X.;
RT "Disabled-2 inactivation is an early step in ovarian tumorigenicity.";
RL Oncogene 18:3103-3113(1999).
RN [4]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
RC TISSUE=Ovary;
RX MEDLINE=98281865; PubMed=9620555;
RA Mok S.C., Chan W.Y., Wong K.-K., Cheung K.K., Lau C.C., Ng S.W.,
RA Baldini A., Colitti C.V., Rock C.O., Berkowitz R.S.;
RT "DOC-2, a candidate tumor suppressor gene in human epithelial ovarian
RT cancer.";
RL Oncogene 16:2381-2387(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 44-304 FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=94148289; PubMed=8314147;
RA Mok S.C., Wong K.-K., Chan R.K.W., Lau C.C., Tsao S.-W., Knapp R.C.,
RA Berkowitz R.S.;
RT "Molecular cloning of differentially expressed genes in human
RT epithelial ovarian cancer.";
RL Gynecol. Oncol. 52:247-252(1994).
CC -!- FUNCTION: Component of the CSF-1 signal transduction pathway (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P98082-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P98082-2; Sequence=VSP_004181;
CC -!- TISSUE SPECIFICITY: Expressed in deep invaginations, inclusion

```

CC cysts and the surface epithelial cells of the ovary. Also
CC expressed in breast epithelial cells, spleen, thymus, prostate,
CC testis, macrophages, fibroblasts, lung epithelial cells, placenta,
CC brain stem, heart and small intestine.
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: Contains 1 PID domain.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; U39050; AAC50824.1; -;
CC EMBL; U41111; AAB19032.1; -;
CC EMBL; AF205890; AAF23161.1; -;
CC EMBL; AF188298; AAF05540.1; -;
CC EMBL; U53446; AAA98975.1; -;
CC EMBL; BC003064; AAH03064.1; -;
CC EMBL; L16886; AAA93195.1; -;
CC PIR; G02228; G02228.
CC Genew; HGNC:2662; DAB2.

CC MIM; 601236; -;
CC GO; GO:0008283; P:cell proliferation; TAS.
CC InterPro; IPR006020; PTB_PID.
CC Pfam; PF00640; PID; 1.
CC SMART; SM00462; PTB; 1.
CC PROSITE; PS01179; PID; 1.
CC Alternative splicing; Phosphorylation.

FT DOMAIN 45 196 PID
FT VARSPPLIC 230 447 Missing (in isoform 2).
FT /FTID=VSP_004181.
FT CONFLICT 44 47 KGDG -> PRVC (IN REF. 6).
FT CONFLICT 82 82 R -> A (IN REF. 3 AND 5).
FT CONFLICT 148 148 A -> T (IN REF. 4).
FT CONFLICT 197 197 M -> R (IN REF. 4).
FT CONFLICT 209 229 MISSING (IN REF. 3).
FT CONFLICT 230 232 ESK -> VCF (IN REF. 3 AND 6).
FT CONFLICT 275 275 S -> L (IN REF. 3, 4 AND 5).
FT CONFLICT 302 304 QPD -> HTR (IN REF. 6).
FT CONFLICT 498 498 L -> Q (IN REF. 3).
SQ SEQUENCE 770 AA; 82506 MW; 317EF3F1343AFEAF CRC64;

Query Match 31.7%; Score 44; DB 1; Length 770;
Best Local Similarity 41.7%; Pred. No. 83;
Matches 10; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 2 RPWTNCSLDGRSVL--KTGTTEKD 23
Db 92 RIWNISLSGIKIIDEKTGVIEH 115

RESULT 39

YU30 RALSO
ID YU30 RALSO STANDARD; PRT; 1582 AA.
AC Q8XV02;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0192 protein RSC3030 precursor.
GN RSC3030 OR RS04727.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT Genome sequence of the plant pathogen Ralstonia solanacearum.;
RL Nature 415:497-502(2002).

CC -!- SIMILARITY: Belongs to the UPF0192 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; AL646073; CAD16739.1; -;
CC InterPro; IPR008930; Terp_cyc_toroid.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 1582 HYPOTHETICAL PROTEIN RSC3030.
SQ SEQUENCE 1582 AA; 170090 MW; 8683D148F5AE3C2A CRC64;

Query Match 31.7%; Score 44; DB 1; Length 1582;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 4 WTNCSLDGRSVLKTGTTEKD 23
Db 278 WT----DGVGVLASGTTQAD 293

RESULT 40

YHGH_ECOLI
ID YHGH_ECOLI STANDARD; PRT; 227 AA.
AC P46846;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yhgh.
GN YHGH OR B3413.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KL12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SIMILARITY: TO H.INFLUENZAE COMF AND B.SUBTILIS COMFC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; U18997; AAA58211.1; ALT INIT.
DR EMBL; AE000417; AAC76438.1; ALT_INIT.
DR EcoGene; EGI2934; yhgH.
DR InterPro; IPR005222; ComF.
DR InterPro; IPR000836; PRTransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR00201; comF; 1.
KW Hypothetical protein; Complete proteome.

FT DOMAIN 8 54 CYS-RICH.
SQ SEQUENCE 227 AA; 25726 MW; BA8768610CDA03BE CRC64;
Query Match 31.3%; Score 43.5; DB 1; Length 227;
Best Local Similarity 34.8%; Pred. No. 26; -
Matches 8; Conservative 4; Mismatches 8; Indels 3; Gaps 1;
Qy 1 CRP---WTNCSLDGRSVLKTGTT 20
Db 138 COPLSRWLHCQWDSEAVTRTRAT 160

Search completed: May 5, 2004, 14:38:41
Job time : 1.96918 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:21 ; Search time 8.56164 Seconds
(without alignments)
921.313 Million cell updates/sec

Title: US-10-067-122B-2_COPY_133_157
Perfect score: 139
Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	139	100.0	211	11	Q8R037	Q8R037 mus musculus
2	75	54.0	267	6	O02764	O02764 oryctolagus
3	66	47.5	274	6	Q7YRL5	Q7YRL5 canis famil
4	63	46.8	278	6	Q8SQ34	Q8SQ34 sus scrofa
5	63	45.3	223	4	Q86YK5	Q86YK5 homo sapien
6	62	44.6	289	11	Q8K2X6	Q8K2X6 mus musculus
7	57	41.0	277	6	Q8WMQ2	Q8WMQ2 ovine aries
8	57	41.0	483	13	Q800K7	Q800K7 paralicththy
9	54.5	39.2	196	11	Q8VC17	Q8VC17 mus musculus
10	54.5	39.2	232	16	Q88PW0	Q88PW0 pseudomonas
11	54.5	39.2	275	11	Q80WM9	Q80WM9 mus musculus
12	53.5	38.5	772	17	Q9UYF4	Q9UYF4 pyrococcus
13	51	36.7	138	10	Q7XBZ5	Q7XBZ5 oryza sativ
14	51	36.7	191	10	Q8S7E9	Q8S7E9 oryza sativ
15	51	36.7	276	13	Q9DDD2	Q9DDD2 gallus gall
16	51	36.7	810	5	O61228	O61228 tenebrio mo

17	51	36.7	3025	2	Q846X6	Q846X6 streptomyce
18	50	36.0	230	10	Q9M2A5	Q9M2A5 arabidopsis
19	50	36.0	279	11	Q8K2X7	Q8K2X7 mus musculus
20	50	36.0	354	10	Q9M365	Q9M365 arabidopsis
21	50	36.0	363	16	Q82WA1	Q82WA1 nitrosomona
22	50	36.0	378	16	Q7VQA7	Q7VQA7 candidatus
23	49.5	35.6	170	10	Q9SX68	Q9SX68 arabidopsis
24	49	35.3	360	2	Q8RS35	Q8RS35 pseudomonas
25	48.5	34.9	766	17	O58222	O58222 pyrococcus
26	48.5	34.9	1076	5	Q9W2P1	Q9W2P1 drosophila
27	48.5	34.9	1141	5	Q8MLX0	Q8MLX0 drosophila
28	48	34.5	115	16	Q8Y8W2	Q8Y8W2 listeria mo
29	48	34.5	250	11	Q8C4K3	Q8C4K3 mus musculus
30	48	34.5	296	5	Q9N2W8	Q9N2W8 caenorhabdi
31	48	34.5	651	13	Q98SM6	Q98SM6 gallus gall
32	48	34.5	1006	16	Q87IL5	Q87IL5 vibrio para
33	47.5	34.2	415	5	Q8SYT9	Q8SYT9 drosophila
34	47.5	34.2	616	5	Q9V690	Q9V690 drosophila
35	47	33.8	119	16	P73915	P73915 synechocyst
36	47	33.8	229	11	Q8BJV0	Q8BJV0 mus musculus
37	47	33.8	231	16	Q97EL8	Q97EL8 clostridium
38	47	33.8	306	16	Q8PIF1	Q8PIF1 xanthomonas
39	47	33.8	350	10	Q9FGB8	Q9FGB8 arabidopsis
40	47	33.8	364	16	Q9PES8	Q9PES8 xylella fas
41	47	33.8	364	16	Q87AS4	Q87AS4 xylella fas
42	47	33.8	369	16	Q8PPE0	Q8PPE0 xanthomonas
43	47	33.8	557	12	Q9J2L5	Q9J2L5 macaca mula
44	47	33.8	559	3	Q8X0Z7	Q8X0Z7 candida gla
45	47	33.8	567	11	Q99J43	Q99J43 mus musculus

ALIGNMENTS

RESULT 1

Q8R037 ID Q8R037 PRELIMINARY; PRT; 211 AA.

AC Q8R037; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Similar to tumor necrosis factor receptor superfamily, member 9.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028507; AAH28507.1; -

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 1.

DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS01186; EGF 2; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

KW Receptor..

SQ SEQUENCE 211 AA; 22452 MW; 1EECA84EA32A8D50 CRC64;

Query Match 100.0%; Score 139; DB 11; Length 211;
Best Local Similarity 100.0%; Pred. No. 6.8e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 2
O02764


```

DR PROSITE; PS00215; MITOCH_CARRIER; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
FT NON_TER      223      223
SQ SEQUENCE     223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match          45.3%; Score 63; DB 4; Length 223;
Best Local Similarity 44.0%; Pred. No. 0.099;
Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDWV 25
   |||||:| | :| | :| |
Db 161 CFPWTSCETKDLVVQQAGTNKTDW 185

RESULT 6
ID Q8K2X6 PRELIMINARY; PRT; 289 AA.
AC Q8K2X6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC029254; AAR29254.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_C6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SMO0208; TNFR; 4.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE     289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;

Query Match          44.6%; Score 62; DB 11; Length 289;
Best Local Similarity 40.0%; Pred. No. 0.19;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
   |||||:| | :| | :| |
Db 161 CYPWTSCEKNLEVLQKGTSQTNI 185

RESULT 7
ID Q8WMQ2 PRELIMINARY; PRT; 277 AA.
AC Q8WMQ2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```


OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248288; CAB50458.1; -
DR PIR; D75002; D75002.
DR HSSP; Q56310; IB3Q.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR002545; Chew.
DR InterPro; IPR004105; H-kinase_dim.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR008207; Hpt.
DR InterPro; IPR008208; Hpt_N.
DR Pfam; PF01584; Chew; 1.
DR Pfam; PF02895; H-kinase_dim; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF01627; Hpt; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD003142; Hpt_N; 1.
DR SMART; SM00260; Chew; 1.
DR SMART; SM00073; HATPase_c; 1.
DR SMART; SM00073; HPT; 1.
DR PROSITE; PS50851; CHEW; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50894; HPT; 1.
KW Kinase; Complete proteome.
SQ SEQUENCE 772 AA; 86113 MW; 314766A6CAD2108B CRC64;

Query Match 38.5%; Score 53.5; DB 17; Length 772;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 5; Mismatches 4; Indels 3; Gaps 1;

QY 4 WTNCSLDGRSVLKTGTTEKDVV 25
Db 207 WTN---PGRDVIESGNLDKQVI 225
||| |||:|:|:|

RESULT 13
QYXBZ5 PRELIMINARY; PRT; 138 AA.
AC QYXBZ5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0057L21.8.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice chromosome 10."
RL Science 300:1566-1569 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
DR EMBL; AJ293700; CAC20218.1; -
DR HSSP; Q92956; 1JMA.

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017121; AAP55081.1; -
KW Hypothetical protein.
SQ SEQUENCE 138 AA; 15173 MW; 0627C2D8842A1757 CRC64;

Query Match 36.7%; Score 51; DB 10; Length 138;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGR 12
Db 78 CRPWRLCSVDPR 89
||| |||:|:|

RESULT 14
QYXBZ5 PRELIMINARY; PRT; 191 AA.
AC QYXBZ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN OSJNBA0057L21.8.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J., Salzberg S.L., White O., Fraser C.M.;
RA "Oryza sativa chromosome 10 BAC OSJNBA0057L21 genomic sequence."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC087599; AAL79707.1; -
DR Gramene; Q897E9; -
KW Hypothetical protein.
FT NON TER. 1
SQ SEQUENCE 191 AA; 20559 MW; C4C856D83BC4E14B CRC64;

Query Match 36.7%; Score 51; DB 10; Length 191;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGR 12
Db 131 CRPWRLCSVDPR 142
||| |||:|:|

RESULT 15
QYXBZ5 PRELIMINARY; PRT; 276 AA.
AC QYXBZ5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Human CD40-homologue.
GN TNPSF5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregaskes C.A.;
RL Thesis (2001); University of Reading, Reading, UNITED KINGDOM.
DR EMBL; AJ293700; CAC20218.1; -
DR HSSP; Q92956; 1JMA.

DR GO:0016020; C:membrane; IEA.
 DR GO:0005634; C:nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR GO:0007165; P:signal transduction; IEA.
 DR InterPro: IPR008063; Fas_receptor.
 DR InterPro: IPR001005; Myb_DNA_binding.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR PRINTS: PR01680; FASRECEPTOR.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00037; MYB_1; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 3.
 SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

Query Match 36.7%; Score 51; DB 13; Length 276;
 Best Local Similarity 40.0%; Pred. No. 10;
 Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
 |||||
 Db 162 CHFWTSCCEKGLVVKVKGNTSDVI 186
 |||||

RESULT 16
 O61228 PRELIMINARY; PRT; 810 AA.
 AC O61228;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Thr4 protein.
 GN THR4.
 OS Tenebrio molitor (Yellow mealworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99449601; PubMed=10518792;
 RA Mouillet J.F., Bousquet F., Sedano N., Alabouvette J., Nicolai M.,
 RA Zelus D., Laudet V., Delachambre J.;
 RT "Cloning and characterization of new orphan nuclear receptors and
 RT their developmental profiles during Tenebrio metamorphosis.";
 RL Eur. J. Biochem. 265:972-981(1999).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 DR EMBL: AJ005685; CAA06670.1; -.
 DR HSSP: P19793; 2NLL.
 DR GO:0005634; C:nucleus; IEA.
 DR GO:0003707; F:steroid hormone receptor activity; IEA.
 DR GO:0003700; F:transcription factor activity; IEA.
 DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO:0006350; P:transcription; IEA.
 DR InterPro: IPR000536; Hormone_rec_lig.
 DR InterPro: IPR001723; Stdhrmn_receptor.
 DR InterPro: IPR008946; Str_ncl_receptor.
 DR InterPro: IPR001628; Znf_C4steroid.
 DR Pfam: PF00104; hormone_rec; 1.
 DR Pfam: PF00105; zf-C4; 1.
 DR PRINTS: PR00398; STRDHORMONER.
 DR PRINTS: PR00047; STROIDFINGER.
 DR ProDom: PD000035; Znf_C4steroid; 1.
 DR SMART: SM00430; HOLI_1.
 DR SMART: SM00399; Znf_C4; 1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 810 AA; 89535 MW; A55D987DFC7F489 CRC64;

QY 5-TNCSLDGRSVLKTGTTEKDVV 25
 :|||
 Db 28 SRCSSDGEVADTSTSSPDV 48
 :|||

RESULT 17
 Q846X6 PRELIMINARY; PRT; 3025 AA.
 ID Q846X6;
 AC Q846X6;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Monensin polyketide synthase loading module and module 1.
 GN MONAI.
 OS Streptomyces cinnamonensis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC15413;
 RA Olinyk M., Olinyk Z.V., Leadlay P.F.;
 RT "The gene cluster for monensin biosynthesis.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC15413;
 RA Olinyk M.;
 RT "The gene cluster for monensin biosynthesis.";
 RL Thesis (1999), University of Cambridge, U.K.
 DR EMBL: AF440781; AAC65796.1; -.
 DR GO:0016020; C:membrane; IEA.
 DR GO:0016740; F:transferase activity; IEA.
 DR GO:0005215; F:transporter activity; IEA.
 DR GO:0006633; P:fatty acid biosynthesis; IEA.
 DR GO:0008152; P:metabolism; IEA.
 DR GO:0006810; P:transport; IEA.
 DR InterPro: IPR001227; AC_trans.
 DR InterPro: IPR000515; BPD_transp.
 DR InterPro: IPR000794; Ketoacyl synth.
 DR InterPro: IPR006162; Ppantne_S.
 DR InterPro: IPR006163; Pp_bind.
 DR Pfam: PF00698; Acyl_transf; 2.
 DR Pfam: PF00109; ketoacyl-synt; 2.
 DR Pfam: PF02801; ketoacyl-synt_C; 2.
 DR Pfam: PF00550; pp-binding; 2.
 DR PROSITE: PS00075; ACP_DOMAIN; 2.
 DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; 1.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; 2.
 SQ SEQUENCE 3025 AA; 312521 MW; 6F4BC965DAB19F25 CRC64;

Query Match 36.7%; Score 51; DB 2; Length 3025;
 Best Local Similarity 54.5%; Pred. No. 1.5e+02;
 Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

QY 3 PWTNCSLDGRSVLK-TGTTEKD 23
 |||||
 Db 2110 PWT-CHADGRVLAETGTASED 2130
 :|||

RESULT 18
 Q9M2A5 PRELIMINARY; PRT; 230 AA.
 ID Q9M2A5;
 AC Q9M2A5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

```

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN F15G16.120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN [2]
SEQUENCE FROM N.A.
RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RRL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132959; CAB71103.1; -.
DR PIR; T47965; T47965.
KW Hypothetical protein.
SQ SEQUENCE 354 AA; 39750 MW; 3BC6D1190885CF8C CRC64;

Query Match 36.0%; Score 50; DB 10; Length 354;
Best Local Similarity 52.4%; Pred.No. 20;
Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 4 WTNCs--LDGRSVLKTGTTEK 22
Db 93 WTYISRFLDGKSLVKGATNK 113

RESULT 21
Q82WA1
ID Q82WA1 PRELIMINARY; PRT; 363 AA.
AC Q82WA1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Riboflavin biosynthesis bifunctional RibD (EC 3.5.4.26).
GN RIBD OR NE0793.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RN [2]
SEQUENCE FROM N.A.
RA STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RA "Complete genome sequence of the ammonia-oxidizing bacterium and
RT Obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321858; CAD94704.1; -.
DR GO; GO:0008703; F:5-amino-6-(5-phosphoribosylamino)uracil red. .; IEA.
DR GO; GO:0008835; F:diaminohydroxyphosphoribosylaminopyrimidine. .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009231; P:vitamin B2 biosynthesis; IEA.
DR InterPro; IPR002125; dCMP/cyt deam.
DR InterPro; IPR004794; Eubact_ribD.
DR InterPro; IPR002734; RibD_C.
DR Pfam; PF00383; dCMP_cyt_deam; 1.
DR Pfam; PF01872; RibD_C; 1.
DR TIGRFAMS; TIGR00326; eubact_ribD; 1.
DR TIGRFAMS; TIGR00227; ribD_Cterm; 1.
DR PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 363 AA; 39834 MW; 38E50089EA2276BB CRC64;

Query Match 36.0%; Score 50; DB 16; Length 363;
Best Local Similarity 41.7%; Pred.No. 20;

```


Q9W2P1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CG3216 protein.
CG3216.
Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RC MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003452; AAF46649.1; -.
DR HSSP; P26769; 1AB8.
DR FlyBase; FBgn0034568; CG3216.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004383; F:guanylate cyclase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008528; F:peptide receptor activity, G-protein coupled; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0008075; F:receptor guanylate cyclase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR001054; G_cyclase.
DR InterPro; IPR001170; Ntpep_receptorN.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00211; Guanylate_cyc; 1.

```

DR Pfam; PF00069; pkinase; 2.
DR PRINTS; PR00255; NATPEPTIDER.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00044; CYCC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SQ SEQUENCE 1076 AA; 121741 MW; 381AA9D3402C7062 CRC64;

Query Match          34.9%; Score 48.5; DB 5; Length 1076;
Best Local Similarity 48.1%; Pred. No. 1.2e+02;
Matches 13; Conservative 1; Mismatches 6; Indels 7; Gaps 1;

QY 6 NCSDGSRVSK-----TGTEKDVV 25
||| ||| ||| ||| ||| ||| |||
Db 677 NCLDGRFVLKISDFGLRLTTPSDFV 703

RESULT 27
Q8MLX0 PRELIMINARY; PRT; 1141 AA.
AC Q8MLX0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG3216-PB.
GN CG3216.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch L., Baldwin D.,
RA Ballew R.M., Basu P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Borkov D., Botchan M.R., Bouck J., Brockstein P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle B.J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

```

```

RT "The genome sequence of Drosophila melanogaster.";
RL Science.287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreria S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacle B.J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Ciamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003452; AAM68187.1; -
DR FlyBase; FBgn0034568; CG3216.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004383; F:guanylate cyclase activity; IEA.
DR GO; GO:0016829; F:peptide receptor activity; IEA.
DR GO; GO:0008528; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004713; F:receptor guanylate cyclase activity; IEA.
DR GO; GO:0008075; F:transferase activity; IEA.
DR GO; GO:0016740; F:intracellular signaling cascade; IEA.
DR GO; GO:0007242; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR001054; G_cyclase.
DR InterPro; IPR001170; Ntpep_receptorN.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00211; guanylate cyc; 1.
DR Pfam; PF00069; pkinase; 2.
DR PRINTS; PR00255; NATPEPTIDER.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00044; CYCC; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SQ SEQUENCE 1141 AA; 128803 MW; 339994FE2354564E CRC64;

Query Match          34.9%; Score 48.5; DB 5; Length 1141;
Best Local Similarity 48.1%; Pred. No. 1.3e+02;

```

```

Matches 13; Conservative 1; Mismatches 6; Indels 7; Gaps 1
QY 6 NCSLDGRSVLK-----TGTTEKDVV 25
DB 742 NCLIDGRFVLKISDFGLRLTLTPSDFV 768

RESULT 28
Q8Y8W2 PRELIMINARY; PRT; 115 AA.
AC Q8Y8W2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein lmo0780.
GN LMO0780.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591976; CAC98858.1; -.
DR PIR; AD1172; AD1172.
DR ListList; LMO00780; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 115 AA; 13425 MW; 3D69674608FD8F9B CRC64;

Query Match 34.5%; Score 48; DB 16; Length 115;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 WTNCSLDGRSVLKT 17
DB 100 WAECCKQKALIKT 113

RESULT 29
Q8C4K3 PRELIMINARY; PRT; 250 AA.
AC Q8C4K3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor superfamily.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).

```

Query Match 34.5%; Score 48; DB 16; Length 1006;
Best Local Similarity 38.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 6; Mismatches 7; Indels

Qy 2 RPWNCSLDGRSVLKTGTTEK 22

[1]
RN .
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,


```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
DR EMBL; AK078859; BAC37424.1; -.
FT NON TER 1
SQ SEQUENCE 229 AA; 24112 MW; 5A1C6870662B95F3 CRC64;

Query Match 33.8%; Score 47; DB 11; Length 229;
Best Local Similarity 32.0%; Pred. No. 37;
Matches 8; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDV 25
DB 1 CQPHTRCEIQGLVEAAPGTSYSDTI 25

RESULT 37
Q97EL8
ID Q97EL8 PRELIMINARY; PRT; 231 AA.
AC Q97EL8;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amidase, germination specific (cwlc/cwid B.subtilis.
DE ortholog).
GN CAC3092.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeischenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007806; AAK81032.1; -.
DR PIR; E97280; E97280.
DR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; Peptidoglycan catabolism; IEA.
DR InterPro; IPR002508; Amidase_3.
DR Pfam; PF01520; Amidase 3; 1.
DR SMART; SM00646; Ami_3; 1.
DR Complete proteome.
SQ SEQUENCE 231 AA; 26138 MW; F9846AF0D4F93351 CRC64;

Query Match 33.8%; Score 47; DB 16; Length 231;
Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTEKDV 24
DB 50 IDGGANLKDGTEKDI 65

RESULT 38
Q8PIF1
ID Q8PIF1 PRELIMINARY; PRT; 306 AA.
AC Q8PIF1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
```

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Thiamine biosynthesis lipoprotein ApbE.
GN APBE OR XAC2947.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011936; AM37792.1; -.
DR GO; GO:0009228; P:thiamin biosynthesis; IEA.
DR InterPro; IPR003374; ApbE.
DR Pfam; PF02424; ApbE; 1.
DR Lipoprotein; Complete proteome.
SQ SEQUENCE 306 AA; 32484 MW; 0D27995DE35520BC CRC64;

Query Match 33.8%; Score 47; DB 16; Length 306;
Best Local Similarity 42.9%; Pred. No. 51;
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 4 WTNCSLDGRSVLKTGTTEKDV 24
DB 117 WQRLQDGRRLVQPGAAALDL 137

RESULT 39
Q9FGB8
ID Q9FGB8 PRELIMINARY; PRT; 350 AA.
AC Q9FGB8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Emb|CAB71103.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026643; BAB09257.1; -.
SQ SEQUENCE 350 AA; 39037 MW; 8FEE77CCA2207AFF CRC64;

Query Match 33.8%; Score 47; DB 10; Length 350;
Best Local Similarity 47.6%; Pred. No. 59;
Matches 10; Conservative 4; Mismatches 5; Indels 2; Gaps 1;
```


QY 4 WTNCs--LDGRSVLKTGTTEK 22
Db 89 WTYITRFELDGKSLVXLGATNK 109

Search completed: May 5, 2004, 14:40:35
Job time : 9.56164 secs

RESULT 40
Q9PES8 PRELIMINARY; PRT; 364 AA.

AC Q9PES8; MEDLINE=20365717; PubMed=10910347;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Riboflavin-specific deaminase.
GN XF0950.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Buenc M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terezzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AE003934; AAF83760.1; -.
DR PIR; G82740; G82740.
DR GO; GO:0008703; F:5-amino-6-(5-phosphoribosylamino)uracil red. . .; IEA.
DR GO; GO:0008835; F:diaminohydroxyphosphoribosylaminopyrimidine. . .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009231; P:vitamin B2 biosynthesis; IEA.
DR InterPro; IPR002125; dCMP/cyt deam.
DR InterPro; IPR004794; Eubact ribD.
DR InterPro; IPR002734; RibD_C.
DR Pfam; PF00383; dCMP_cyt_deam; 1.
DR Pfam; PF01872; RibD_C; 1.
DR TIGRFAMS; TIGR00326; eubact ribD; 1.
DR TIGRFAMS; TIGR00227; ribD Cterm; 1.
DR PROSITE; PS00903; CYT_DCMF_DEAMINASES; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 38751 MW; C5B16D70802D293B CRC64;

Query Match 33.8%; Score 47; DB 16; Length 364;
Best Local Similarity 41.7%; Pred. No. 61;
Matches 10; Conservative 4; Mismatches 6; Indels 4; Gaps 1;
QY 2 RPWT----NCSLDGRSVLKTGTTE 21

This Page Blank (uspio)